

SEQUENCE LISTING

<110> Sagami Chemical Research Center,
Protegene Inc.

<120> HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE
PROTEINS

<130> GIN-6727CPUS

<150> JP 10-326255

<151> 1998-11-17

<150> JP 10-364315

<151> 1998-12-22

<150> JP 11-69111

<151> 1999-03-16

<150> JP 11-119299

<151> 1999-04-27

<150> JP 11-134169

<151> 1999-06-19

<160> SEQ

<210> 1

<211> 647

<212> PRT

<213> Homo sapiens

<400> 1

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Met Ala Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly Gly Gly
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Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu Thr Glu
 20          25          30
Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val Asp Pro
 35          40          45
Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Trp Leu Leu Glu Ala
 50          55          60
Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly Pro Gly
 65          70          75          80
Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Gln Gln Gln
 85          90          95
Gln Ser Gly Gln Gln Tyr Asn Gly Gln Arg Gly Ile Ser Val Pro Asp
100          105          110
His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala
115          120          125
Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu
130          135          140
Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln
145          150          155          160
Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val
165          170          175
Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu
180          185          190
Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln
195          200          205
Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly Ala Gly
210          215          220

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Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro Thr Pro
 225 230 235 240
 Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly Gly Gly
 245 250 255
 Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu Arg Gly
 260 265 270
 Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu Asn Tyr
 275 280 285
 His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro Thr Lys
 290 295 300
 Val Tyr Gly Leu Met Tyr Phe Gly Pro Gln Glu Leu Arg Phe Ser Arg
 305 310 315 320
 Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr Leu Phe
 325 330 335
 Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr Pro Gln
 340 345 350
 Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala Val Ala
 355 360 365
 Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn Asp Lys
 370 375 380
 Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys Lys Glu
 385 390 395 400
 Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met Ala Ser
 405 410 415
 Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly
 420 425 430
 Met Lys Trp Gly His Gln Ala Ile Glu Ala Asn Ser Gln Tyr Phe His
 435 440 445
 Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile Leu Ala
 450 455 460
 Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe Val Gly
 465 470 475 480
 Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro Leu Phe
 485 490 495
 Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe Val Ser
 500 505 510
 Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys Thr Gln
 515 520 525
 Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val Leu Tyr
 530 535 540
 Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Gln Gln Ala
 545 550 555 560
 Phe Arg Asp Gln Trp Gln Arg Ser Trp Val Ala Gln Ser Cys Lys Ser
 565 570 575
 Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala Pro Pro
 580 585 590
 His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys Tyr Leu
 595 600 605
 Met Thr Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp Ser Gly
 610 615 620
 Lys Thr Leu Asn Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr Asn Ser
 625 630 635 640
 Lys Gln Gly Glu Thr Val
 645

<210> 2

<211> 350

<212> PRT

<213> Homo sapiens

<400> 2

Met His Pro Ala Ala Phe Pro Leu Pro Val Val Val Ala Ala Val Leu
1 5 10 15
Trp Gly Ala Ala Pro Thr Arg Gly Leu Ile Arg Ala Thr Ser Asp His
20 25 30
Asn Ala Ser Met Asp Phe Ala Asp Leu Pro Ala Leu Phe Gly Ala Thr
35 40 45
Leu Ser Gln Gln Gly Leu Gln Gly Phe Leu Val Gln Ala His Pro Asp
50 55 60
Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro Ala Pro Val Asn Gly
65 70 75
Ser Val Phe Ile Ala Leu Leu Arg Arg Phe Asp Cys Asn Phe Asp Leu
80 85 90 95
Lys Val Leu Asn Ala Gln Lys Ala Gly Tyr Gly Ala Ala Val Val His
100 105 110
Asn Val Asn Ser Asn Gln Leu Leu Asn Met Val Trp Asn Ser Gln Gln
115 120 125
Ile Gln Gln Gln Ile Trp Ile Pro Ser Val Phe Ile Gly Gln Arg Ser
130 135 140
Ser Gln Tyr Leu Arg Ala Leu Phe Val Tyr Gln Lys Gly Ala Arg Val
145 150 155 160
Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr Leu Ile Pro
165 170 175
Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly Ala Val Met
180 185 190
Ile Ala Arg Cys Ile Gln His Arg Lys Arg Leu Gln Arg Asn Arg Leu
195 200 205
Thr Lys Gln Gln Leu Lys Gln Ile Pro Thr His Asp Tyr Gln Lys Gly
210 215 220
Asp Gln Tyr Arg Val Cys Ala Ile Cys Leu Asp Gln Tyr Gln Asp Gly
225 230 235 240
Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His Ser Arg Cys
245 250 255
Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro Ile Cys Lys
260 265 270
Gln Pro Val His Arg Gly Pro Gly Asp Gln Asp Gln Gln Gln Thr
275 280 285
Gln Gly Gln Ser Gln Gly Asp Gln Gly Gln Pro Arg Asp His Pro Ala
290 295 300
Ser Gln Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu Pro Thr Ser
305 310 315 320
Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly Pro Ser Thr
325 330 335
Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu Val
340 345 350

0110 -

0111 - L06

0112 - PRT

0113 - Homo sapiens

0100 -

Met Gly Leu Gly Gln Pro Gln Ala Trp Leu Leu Gly Leu Pro Thr Ala
1 5 10 15
Val Val Tyr Gly Ser Leu Ala Leu Phe Thr Thr Ile Leu His Asn Val
20 25 30
Phe Leu Leu Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn
35 40 45
Lys Met Ala Phe Trp Val Gly Gln Thr Val Phe Leu Leu Trp Asn Ser
50 55 60
Leu Asn Asp Pro Leu Phe Gly Trp Leu Ser Asp Arg Gln Phe Leu Ser
65 70 75 80

Ser Gln Pro Arg Gly Arg Asp Leu Pro Trp Leu Gly Leu Val Gly Pro
85 90 95
Ser Gly Leu Trp Thr Ala Asn Thr Leu Cys Cys Phe Trp Lys Ile Pro
100 105 110
Leu Pro His Pro Cys Leu Ser Pro Ser Ser Pro Pro Thr Leu Arg Ser
115 120 125
Gly His Pro Ile Pro Phe Gly His Gln Pro Asn Arg Leu Ile Arg Gly
130 135 140
Trp Lys Leu Gly Gln Arg Arg Val Tyr Pro Leu Val Arg Arg Arg
145 150 155 160
Ala Leu Leu Lys Gly Cys Gly Ala Gly Pro Gly Ala Gly Pro Gly Leu
165 170 175
Ala Trp Ala Ala Ala Gly Ala Val Val Pro Gly Val Leu Gly Ala Leu
180 185 190
Gly Pro Ser Trp Pro Ala Val Leu Ala Val Pro Val Pro Leu
195 200 205

<210> 4

<211> 213

<212> PRT

<213> Homo sapiens

<400> 4

Met His Tyr Tyr Arg Tyr Ser Asn Ala Lys Val Ser Cys Trp Tyr Lys
1 10 15
Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly Val Val
20 25 30
Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val Leu Ser
35 40 45
Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Val Val Leu
50 55 60
Val Leu Met Val Gly Val Val Met Phe Thr Leu Gly Phe Ala Gly Cys
65 70 75 80
Val Gly Ala Leu Arg Glu Asn Ile Cys Leu Leu Asn Phe Asn Gln Cys
85 90 95
Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr Phe Asn
100 105 110
Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser
115 120 125
Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly
130 135 140
Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser Ile Phe
145 150 155 160
Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile
165 170 175
Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe
180 185 190
Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys
195 200 205
Ala Gly His His Phe
210

<210> 5

<211> 595

<212> PRT

<213> Homo sapiens

<400> 5

Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln Leu Leu Leu Leu
1 5 10 15
Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu Ser Pro Leu Pro Ala



Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
 515 520 525
 Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
 530 535 540
 Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly
 545 550 555 560
 Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Arg
 565 570 575
 Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu Gln Pro Gln Pro Arg
 580 585 590
 Asp Glu Leu
 595

0108 6
 0111 264
 0112 PRT
 0113 Homo sapiens

0400 6
 Met Val Ala Ser Ala Lys Met Gly Arg Ala Gly Thr Met Ala Val Ala
 1 5 10 15
 Ala Glu Leu Arg Glu Leu Cys Pro Gly Val Asn Asn Gln Pro Tyr Leu
 20 25 30
 Cys Glu Ser Gly His Cys Cys Gly Glu Thr Gly Cys Cys Thr Tyr Tyr
 35 40 45
 Tyr Glu Leu Trp Trp Phe Trp Leu Leu Trp Thr Val Leu Ile Leu Phe
 50 55 60
 Ser Cys Cys Cys Ala Phe Arg His Arg Arg Ala Lys Leu Arg Leu Gln
 65 70 75 80
 Gln Gln Gln Arg Gln Arg Gly Ile Asn Leu Leu Ala Tyr His Gly Ala
 85 90 95
 Cys His Gly Ala Gly Pro Phe Pro Thr Gly Ser Leu Leu Asp Leu Arg
 100 105 110
 Phe Leu Ser Thr Phe Lys Pro Pro Ala Tyr Glu Asp Val Val His Arg
 115 120 125
 Pro Gly Thr Pro Pro Pro Pro Tyr Thr Val Ala Pro Gly Arg Pro Leu
 130 135 140
 Thr Ala Ser Ser Glu Gln Thr Cys Cys Ser Ser Ser Ser Ser Cys Pro
 145 150 155 160
 Ala His Phe Glu Gly Thr Asn Val Glu Gly Val Ser Ser His Gln Ser
 165 170 175
 Ala Pro Pro His Gln Glu Gly Glu Pro Gly Ala Gly Val Thr Pro Ala
 180 185 190
 Ser Thr Pro Pro Ser Cys Arg Tyr Arg Arg Leu Thr Gly Asp Ser Gly
 195 200 205
 Ile Glu Leu Cys Pro Cys Pro Ala Ser Gly Glu Gly Glu Pro Val Lys
 210 215 220
 Glu Val Arg Val Ser Ala Thr Leu Pro Asp Leu Glu Asp Tyr Ser Pro
 225 230 235 240
 Cys Ala Leu Pro Pro Glu Ser Val Pro Gln Ile Phe Pro Met Gly Leu
 245 250 255
 Ser Ser Ser Gln Gly Asp Ile Pro
 260

0108 7
 0111 343
 0112 PRT
 0113 Homo sapiens

0400 7
 Met Gln Pro Pro Pro Pro Gly Pro Leu Gly Asp Cys Leu Arg Asp Trp

1	5	10	15
Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile Gln Glu Thr His Arg Leu			
20	25	30	
Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys Leu Gln Asn Asn Cys Thr			
35	40	45	
Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu Gln Glu Leu Ala Leu Ala			
50	55	60	
Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala Glu Ala Glu Gly Ala Ala			
65	70	75	80
Gln Glu Leu Glu Asn Gln Met Lys Glu Arg Gln Gly Leu Phe Phe Asp			
85	90	95	
Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly Leu Tyr Leu Ser Leu Val			
100	105	110	
Leu Gly Asn Val Asn Val Thr Leu Leu Ser Lys Gln Ala Lys Phe Ala			
115	120	125	
Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu Tyr Leu Thr Ile Ile Leu			
130	135	140	
Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu Leu Asn Ser Arg Val Thr			
145	150	155	160
Asp Ala Ala Phe Asn Phe Leu Leu Val Trp Tyr Tyr Cys Thr Leu Thr			
165	170	175	
Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly Ser Arg Ile Lys Gly Trp			
180	185	190	
Trp Val Phe His His Tyr Val Ser Thr Phe Leu Ser Gly Val Met Leu			
195	200	205	
Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys Phe Arg Asn Gln Phe Leu			
210	215	220	
Ser Phe Ser Met Tyr Gln Ser Phe Val Gln Phe Leu Gln Tyr Tyr Tyr			
225	230	235	240
Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala Leu Gly Glu Arg His Thr			
245	250	255	
Met Asp Leu Thr Val Glu Gly Phe Gln Ser Trp Met Trp Arg Gly Leu			
260	265	270	
Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly His Phe Trp Gln Leu Phe			
275	280	285	
Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln Asp Pro Gln Cys Lys Glu			
290	295	300	
Trp Gln Val Leu Met Cys Gly Phe Pro Phe Leu Leu Leu Phe Leu Gly			
305	310	315	320
Asn Phe Phe Thr Thr Leu Arg Val Val His His Lys Phe His Ser Gln			
325	330	335	
Arg His Gly Ser Lys Lys Asp			
340			

<210> :

<211> 144

<212> PRT

<213> Homo sapiens

<400> :

Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu Thr			
1	5	10	15
Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys			
20	25	30	
Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro Lys Ser Asn			
35	40	45	
Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly			
50	55	60	
Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu Glu Leu Gly Cys Gly			
65	70	75	80
Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys			

	85		90		95
Leu Asp Pro Asn Pro His Phe Glu Lys Phe Leu Thr Lys Ser Met Ala					
	100		105		110
Glu Asn Arg His Leu Gln Tyr Glu Arg Phe Val Val Ala Pro Gly Glu					
	115		120		125
Asp Met Arg Gln Leu Ala Asp Gly Ser Met Asp Val Val Val Cys Thr					
	130		135		140
Leu Val Leu Cys Ser Val Gln Ser Pro Arg Lys Val Leu Gln Glu Val					
	145		150		155
Arg Arg Val Leu Arg Pro Gly Gly Val Leu Phe Phe Trp Glu His Val					
	165		170		175
Ala Glu Pro Tyr Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu					
	180		185		190
Pro Thr Trp Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr					
	195		200		205
Trp Lys Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg					
	210		215		220
Gln Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly					
	225		230		235
Lys Ala Val Lys					240

<210> 9

<211> 303

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Leu Lys Leu Lys Asn Val Phe Leu Ala Tyr Phe Leu Val Ser					
1	5		10		15
Ile Ala Gly Leu Leu Tyr Ala Leu Val Gln Leu Gly Gln Pro Cys Asp					
	20		25		30
Cys Leu Pro Pro Leu Arg Ala Ala Ala Glu Gln Leu Arg Gln Lys Asp					
	35		40		45
Leu Arg Ile Ser Gln Leu Gln Ala Glu Leu Arg Arg Pro Pro Pro Ala					
	50		55		60
Pro Ala Gln Pro Pro Glu Pro Glu Ala Leu Pro Thr Ile Tyr Val Val					
	65		70		75
Thr Pro Thr Tyr Ala Arg Pro Leu Trp Val Gln Tyr Pro Gln Asp Val					
	85		90		95
Thr Thr Phe Asn Ile Asp Asp Gln Tyr Leu Leu Gly Asp Ala Leu Leu					
	100		105		110
Val His Pro Val Ser Asp Ser Gly Ala His Gly Val Gln Val Tyr Leu					
	115		120		125
Pro Gly Gln Gly Glu Val Trp Tyr Asp Ile Gln Ser Tyr Gln Lys His					
	130		135		140
His Gly Pro Gln Thr Leu Tyr Leu Pro Val Thr Leu Ser Ser Ile Pro					
	145		150		155
Val Phe Gln Arg Gly Gly Thr Ile Val Pro Arg Trp Met Arg Val Arg					
	165		170		175
Arg Ser Ser Glu Cys Met Lys Asp Asp Pro Ile Thr Leu Phe Val Ala					
	180		185		190
Leu Ser Pro Gln Gly Thr Ala Gln Gly Glu Leu Phe Leu Asp Asp Gly					
	195		200		205
His Thr Phe Asn Tyr Gln Thr Arg Gln Glu Phe Leu Leu Arg Arg Phe					
	210		215		220
Ser Phe Ser Gly Asn Thr Leu Val Ser Ser Ser Ala Asp Pro Glu Gly					
	225		230		235
His Phe Glu Thr Pro Ile Trp Ile Glu Arg Val Val Ile Ile Gly Ala					
	245		250		255
Gly Lys Pro Ala Ala Val Val Leu Gln Thr Lys Gly Ser Pro Glu Ser					

	260		265		270										
Arg	Leu	Ser	Phe	Gln	His	Asp	Pro	Glu	Thr	Ser	Val	Leu	Val	Leu	Arg
	275		280		285										
Lys	Pro	Gly	Ile	Asn	Val	Ala	Ser	Asp	Trp	Ser	Ile	His	Leu	Arg	
	290		295		300										

<210> 10
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 10															
Met	Asp	Lys	Leu	Lys	Lys	Val	Leu	Ser	Gly	Gln	Asp	Thr	Glu	Asp	Arg
1				5					10					15	
Ser	Gly	Leu	Ser	Glu	Val	Val	Glu	Ala	Ser	Ser	Leu	Ser	Trp	Ser	Thr
	20						25						30		
Arg	Ile	Lys	Gly	Phe	Ile	Ala	Cys	Phe	Ala	Ile	Gly	Ile	Leu	Cys	Ser
	35					40						45			
Leu	Leu	Gly	Thr	Val	Leu	Leu	Trp	Val	Pro	Arg	Lys	Gly	Leu	His	Leu
	50					55					60				
Phe	Ala	Val	Phe	Tyr	Thr	Phe	Gly	Asn	Ile	Ala	Ser	Ile	Gly	Ser	Thr
	65				70				75					80	
Ile	Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Arg	Met	Phe	Glu	Pro
			85					90						95	
Thr	Arg	Leu	Ile	Ala	Thr	Ile	Met	Val	Leu	Leu	Cys	Phe	Ala	Leu	Thr
	100						105						110		
Leu	Cys	Ser	Ala	Phe	Trp	Trp	His	Asn	Lys	Gly	Leu	Ala	Leu	Ile	Phe
	115						120						125		
Cys	Ile	Leu	Gln	Ser	Leu	Ala	Leu	Thr	Trp	Tyr	Ser	Leu	Ser	Phe	Ile
	130					135					140				
Pro	Phe	Ala	Arg	Asp	Ala	Val	Lys	Lys	Cys	Phe	Ala	Val	Cys	Leu	Ala
	145					150				155				160	

<210> 11
 <211> 1941
 <212> DNA
 <213> Homo sapiens

<400> 11						
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ggcggggcc	ggcagggtga	ggccggggga	ctggggggc	agggtgtgt	gtgtgtttgg	180
ctgtgtggag	ctcgtgtgt	gtgtgggggc	gggtggcagg	gggggggca	ggggccaggc	240
caggggggc	gggtggggga	gcaacggggc	gggtgggttc	aggagggca	gagcggggag	300
cagtacaac	ggagggggg	catctcgtc	ggagggaag	gtattggca	ggcattcttc	360
atcgggtgt	ggcgggacat	gggtacaac	cagagcatca	ggcggggc	gtgtggggac	420
acgaacagg	aggaggggg	cttggagggt	cagggtttc	acgtctagt	gaaagtggag	480
tggtcgggt	aggtcaagtt	cttctgtgt	tcattgtac	ggcgggtgt	caccgtgtta	540
gagcagggg	tggtgggttc	gggtgggttc	ggaggggc	ggggggagg	ctggagggg	600
ctcatgaaca	agttgggttc	gggtggggca	gagaggtca	aggtgtgag	gttccgggtg	660
caggggggc	ggagggtgt	gtggggggc	aaagggttc	aaaggggca	cccgaggggc	720
tggtgtgttc	ggagggttc	gacagggaac	ctcagggaag	ggggggagg	gcaccgtggc	780
gggttcggc	ggggggggc	gggtggggc	ggagggaag	ttctctggc	ggcggggc	840
aaagtgggt	ctcagggaac	ctcagggaac	ctggggggga	aggaggtgg	ggcagggttc	900
gagcgggca	aggtgtgttc	gtcattgtac	ttggggggc	aggaggtgc	cttctggggc	960
acgtgggttc	gcattgggtc	aggtgtgttc	tggtgtgttc	gggtgttcac	gggtgttcac	1020
taattgttc	acattggggc	cttcagggtc	ggaggggc	ccatcatctt	cttgttcggc	1080
tggtacagg	gggtggggc	ggcctacatc	ggcgggttc	ttctggaaga	ggaggtgttc	1140
tgtaattgaca	agttggggc	ggcggggga	ggcagggttc	ggcaggggca	caaggaggag	1200
gggtgggca	ttctcttcac	gatgtgttc	ttcttcaggc	tggtcaggc	catctgggtg	1260
gtgatgtgt	gggtcaggc	gttctgtggc	gtgtgggcat	agtgggggca	ggaggggcat	1320

gaagccaaact	cacagttatatt	tcacotgggc	gootggggctg	tgccgggcat	caagaccatc	1480
ccatccctgg	cgctgggcca	ggtgggaaggc	gatgtgctga	ggggagtgatg	cttcgtgggg	1481
ccacaaacg	tggaaggct	ggtgggttc	gtgtggggc	ccctcttgc	gtacctgttc	1482
atcggaagc	ccctcttgc	ggcggttc	gtgtgctct	cccgcatccg	caccatcatg	1483
agagagatg	gcacaaagac	cgagaagctg	gagaagctca	tggtgggcat	gggggtcttc	1484
agggtctgt	acactgtgc	agccaccatc	gcacagctc	gctacctcta	cgagcaggcc	1485
tcacggacc	agtgggaag	cagctgggtg	gcccagagct	gcaagagcta	cgctatcccc	1486
tgcttcacc	tcagggggg	cgagggggc	ccggcgccac	cgcccatgag	ccgggacttc	1487
cggtcttca	tgattaaat	ccctatgag	ccgactgtg	gcacacgtc	gggtctctgg	1488
ctctgtccg	gcagacccct	caactccctg	aggaaagtct	acacgaggct	caccaaagc	1489
caacagggg	agactacagt	c				1490

Q110 - 12
Q111 - 1451
Q112 - DNA
Q113 - Homo sapiens

gagacccctg	cagccttccc	gattcctgtg	gttggggggc	ctgtgctgtg	gggagggggc	60
ccgacccggg	ggctcattcg	agcgaactcg	gaaccacaatg	ccagcatgga	ctttgcagac	61
ctcagagcc	tgctgggggc	tcactcgagc	caggaggggc	tcaggggggc	cttcgtggag	62
ctcagccag	acaaatgctg	cagcaccatt	gcccacccac	ccccagcccc	ggtcaatggg	63
tcactcttca	ttcgctgtgt	tcgaaagctc	gactgcaact	tcgacctcaa	ggtcctaaat	64
tcacagagg	ctggatattg	tgccgtctga	gtacacaaatg	tcgaattccaa	tgaaactctg	65
tcacggggt	ggaatagtga	ggaaatccag	cagcagatct	ggatccccgc	tgatcttact	66
agggagaaa	gctccagcta	cttgggtgac	ctctctgtct	acgagaaagg	ggctcgggtg	67
ctcgggttc	cagacaaatc	cttccctctg	ggctattcac	tcctcccttc	cacagggaat	68
cgagcttgc	tgcttttggc	cattggagca	gtaactgata	ctgtttgcat	ccagcaccgg	69
caagcttcc	agggaaatcg	acttaccaaa	gagcgaactga	aacagattcc	tcacacatgac	70
tcacagagg	gagacccagta	tgatgtctgt	gcattctgac	tcgatgaata	tgaggatggg	71
tcacagctgc	gggtactccc	ctgtgctcac	gcctaccaca	gcgctgctg	ggacccctgg	72
tcactcaga	ccgggaagac	ctgcacatt	tgcaagcaga	ctgttcacac	gggtctctgg	73
tcacagccc	agaggaagaa	aactcaaggg	caagagggagg	gtgatgaagg	ggagccaaag	74
tcacacctgc	cttcagaaaag	gaccccaatt	ttgggtctca	gcccacactc	ccccacctcc	75
tcacttctct	cagcccccagc	tcacttctg	tcctctgggc	cttcaacaga	ccccccactg	1490
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Q114 - 14
Q115 - 613
Q116 - DNA
Q117 - Homo sapiens

atggggctgg	gtcagccccca	ggcttgggtg	ctgggtctgc	ccacagctgt	ggtcttatggc	60
tccttggctc	tccttccccc	gctcttgccc	aaggtctctc	tgctctacta	tggtgacacc	61
tcctgtctag	tgtaaacgat	caacaaaatg	gctctctggg	tcggagagac	aggtgtcttc	62
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tcactacccc	caaccttgag	aagtgggcat	ccatccctct	ttggccatca	gcccacacag	66
ctactaaagg	gggtgaaatt	ggggagagg	aggagagctg	acccactggt	cagggtccgg	67
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tcctgctgtg	tgctctca					618

Q118 - 14
Q119 - 649
Q120 - DNA
Q121 - Homo sapiens

Q122 - 14

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agctacaaca	tcatcttctg	gttggctgga	gttgtcttcc	tggagtcgg	gctgtgggca	120
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ctctagaca	cggaggcagt	gaaggccggc	cataccttc			660

c110 - 15

c111 - 1735

c112 - DNA

c113 - Homo sapiens

c400 - 15

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c110 - 16

c111 - 792

c112 - DNA

c113 - Homo sapiens

c400 - 16

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gagactggct	gctgcacctc	ctactatgag	ctctgggtgt	tctggctgct	ctggactgtc	180
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gagccagttc	aggaggtgag	ggttagtgcc	accccgccag	atctggagga	ctactccctg	740
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 <212> DNA
 <213> Homo sapiens

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<210> 18
 <211> 732
 <212> DNA
 <213> Homo sapiens

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cggcttctgg	tggctctctg	agaggacatg	agacagctgg	ctgatggctc	catggatgtg	440
gtggtctgca	ctctgggtgt	gtgtctctgg	cagagcccaa	ggaaggctcc	gcaggagggtc	440
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<210> 19
 <211> 909
 <212> DNA
 <213> Homo sapiens

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<210> 20
 <211> 480
 <212> DNA
 <213> Homo sapiens

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<210> 11
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 <212> DNA
 <213> Homo sapiens

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gagaaagt atg gct gag gag gag ggc cct aag aag tcc cgg gcc gcc ggc 240
Met Ala Glu Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly
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Gly Gly Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu
15 20 25 30
acg gag gag gcc agc ggg gac gcc ggt ggc cgc cgc cgc cgc cca gtt 326
Thr Glu Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val
35 40 45
gac ccc cgg cga tgg ggc cgc cag ctg ctg ctg ctg ctt tgg ctg ctg 374
Asp Pro Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Trp Leu Leu
50 55 60
gag gct cgc ctg ctg ctg ggg gtc cgg gcc cag gcc gcc gcc cag ggg 422
Glu Ala Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly
65 70 75
cca gcc cag ggg ccc ggg cgc ggg cag caa cgc cgc cgc cgc cct cag 470
Pro Gly Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln

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80	85	90	
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Gln Gln Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val			
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Pro Asp His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp			
115 120 125			
atc ggc tac aac cag acc atc atg ccc aac ctg cgc ggc cac acg aac			614
Ile Ala Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn			
130 135 140			
cag gag gac ggc ggc ctg gag gtg cac cag ttc tac cct cta gtg aaa			662
Gln Glu Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys			
145 150 155			
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Val Gln Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala			
160 165 170			
ccc ggc tcc acc gtg cta gag cag acc ctg ccg cgc tgc cgc tcc ctg			758
Pro Val Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu			
175 180 185 190			
tgc gag cgc ggc cgc cag ggc tgc gag ggc ctg atg aac aag tcc ggc			806
Cys Glu Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly			
195 200 205 210			
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Phe Gln Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly			
215 220 225			
gac gag ggc ctg tgc gtc ggc cag aac aag tcc gac aag ggc acc ccc			902
Ala Gly Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro			
230 235 240			
aag ccc tgc ctg ctt cca gag ttc tgc acc agc aac cct cag cgc ggc			950
Thr Pro Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly			
245 250 255			
ggc gga gag cgc cct ggc ggc ttc ccc ggc ggc ggc ggc ggc tgc gag			998
Gly Gly Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu			
260 265 270			
cga ggc aag ttc tcc tgc ccg cgc acc ctg aag ggc ccc tcc tac ctt			1046
Arg Gly Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu			
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Asn Tyr His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro			
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Thr Lys Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe			
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Ser Arg Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr			
325 330 335			
ctc ttc aag gtc ctt acc tac ctg gtg gac atg cgc cgc ttc acc tac			1238
Leu Phe Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr			
340 345 350			
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Pro Glu Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala			
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Val Ala Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn			
370 375 380			
gac aag ttc ggc gag gac ggc gga tgc act gtg ggc cag ggc acc aag			1382
Asp Lys Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys			
385 390 395			
aag gag ggc tgc acc atc ctc ttc atg atg ctc ttc ttc ctc acc atg			1430
Lys Glu Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met			
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 Ala Gly Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr
 435 440 445
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 Phe His Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile
 450 455 460
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 Leu Phe Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe
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 Val Ser Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys
 515 520 525
 acc gag aag ctg gac aag ctc atg gtg cgc att ggc gtc ttc agc gtg 1814
 Thr Glu Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val
 530 535 540
 ctg tac aat gtg cca gcc acc atc gtc atc gcc tgc tac ttc tac gag 1862
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 545 550 555
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 Lys Ser Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala
 575 580 585 590
 ccg ccg cac ccg ccc atg agc ccg gac ttc acc gtc ttc atg att aag 2006
 Pro Pro His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys
 595 600 605
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<213> Homo sapiens

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<221> CDS

<222> (253)...(1305)

<410> 22

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Met His Pro Ala Ala Phe Pro Leu Pro Val Val Val Ala
1 5 10
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Ala Val Leu Trp Gly Ala Ala Pro Thr Arg Gly Leu Ile Arg Ala Thr
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Gly Ala Thr Leu Ser Gln Glu Gly Leu Gln Gly Phe Leu Val Glu Ala
50 55 60
cac cca gac aat gcc tgc agc ctc att gcc cca cca ccc cca gcc ccg 483
His Pro Asp Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro Ala Pro
65 70 75
gtc aat ggg tca gtc ttt att ggg ctg ctt cga aga ttc gac tgc aac 531
Val Asn Gly Ser Val Phe Ile Ala Leu Leu Arg Arg Phe Asp Cys Asn
80 85 90
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Phe Asp Leu Lys Val Leu Asn Ala Gln Lys Ala Gly Tyr Gly Ala Ala
95 100 105
gta gta cac aat gtg aat tcc aat gaa ctt ctg aac atg gtg tgg aat 627
Val Val His Asn Val Asn Ser Asn Glu Leu Leu Asn Met Val Trp Asn

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Ala Arg Val Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr				
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ctc atc cct ttc aca ggg att gtg gga ctg ctg gtt ttg gcc atg gga				819
Leu Ile Pro Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly				
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Gln Lys Gly Asp Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr				
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Glu Asp Gly Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His				
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Ser Arg Cys Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro				
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Ile Cys Lys Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu				
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Glu Gln Thr Gln Gly Gln Glu Gln Gly Asp Gln Gly Glu Pro Arg Asp				
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His Pro Ala Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu				
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Pro Thr Ser Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly				
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Pro Ser Thr Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu				
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141				
150				
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 (212): DNA
 (213): Homo sapiens

(220):
 (221): CDS
 (222): (23): ... (350)

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Gly Ser Leu Ala Leu Phe Thr Thr Ile Leu His Asn Val Phe Leu Leu						
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Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn Lys Met Ala						
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 1212> DNA
 1213> Homo sapiens

1220>
 1221> 703
 1222> 169)... (710)

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1 5 10
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Tyr Lys Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly
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Leu Ser Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Val
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Phe Ser Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr Gln
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asn ile tyr ile val ala gly val phe ile ala ile ser leu leu gln
175      180      185      190
ata ttt ggc atc ttc ctg gca agg acg ctg atc tca gac atc gag gca      696
ile phe gly ile phe leu ala arg thr leu ile ser asp ile glu ala
195      200      205
gtg aag gcc ggc cat cac ttc tgaggagcag agttgagggg ggcagagctga gcc      740
val lys ala gly his his phe
210
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (20)...(1807)

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Leu Leu Leu Leu Leu Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu
15      20      25
tcg ccg ctg ccc gcc gtg gtc att gcc atc ctg gct ggc aat gcc gaa      148
Ser Pro Leu Pro Ala Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu
30      35      40

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Arg Ala Arg Met Ala Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn	
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acc aca gag atg ctg cag gag tgg ctg gag gct gtg ggc gat gac tat	292
Thr Thr Glu Met Leu Gln Glu Trp Leu Ala Val Gly Asp Asp Tyr	
80 85 90	
gct gct gtg gtc tgg agg cct gag ggc gag ccc agg ttc tac cca gat	340
Ala Ala Val Val Trp Arg Pro Gln Gly Glu Pro Arg Phe Tyr Pro Asp	
95 100 105	
gaa gag ggt ccc aag cac tgg acc aaa gaa agg cac bag ttt ctg atg	388
Glu Glu Gly Pro Lys His Trp Thr Lys Glu Arg His Gln Phe Leu Met	
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Glu Leu Lys Gln Gln Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp	
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Tyr Ile Leu Phe Ala Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr	
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Leu Arg Leu Leu Met Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu	
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Gly Tyr Tyr Arg Arg Thr Ala Gln Tyr Phe Pro Thr Lys Asn Arg Gln	
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Ser Leu Arg Ala Gln Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His	
220 225 230 235	
ccc aac tac act tgg cct ttc gac gac atc atc gtc ttc gcc tat gcc	772
Pro Asn Tyr Thr Trp Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala	
240 245 250	
tgc cag gct gct ggg gtc tcc gtc cac gtg tgc aat gag cac cgt tat	820
Cys Gln Ala Ala Gly Val Ser Val His Val Cys Asn Gln His Arg Tyr	
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ggg tac atg aat gtg cgg gtg aaa tcc cac cag ggg ctg gaa gac gag	868
Gly Tyr Met Asn Val Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu	
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Arg Val Asn Phe Ile His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro	
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cgc atg cag gct tta gct cat gtg act cgg ccc tct aag agg ccc agc	964
Arg Met Gln Ala Ser Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser	
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Lys Ile Gly Phe Asp Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro	
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Asp Arg Arg Glu Arg Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser	
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Ile Arg Asn Leu Gly Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr	
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Tyr Ser Ile Trp Glu Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu	
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Val Phe Glu Asp Asp Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu	
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Glu Arg Leu Met Glu Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu	
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Ile Tyr Leu Gly Arg Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val	
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Glu Gly Leu Pro Gly Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu	
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Asp Gln His Pro Asn Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp	
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Ala Gly Asp Ala Glu Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp	
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Gln Pro Gln Pro Arg Asp Glu Leu	
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Thr Gly Cys Cys Thr Tyr Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Leu
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tgg act gtc ctg atc ctg ttt acc tgc tat tgc ggc ttc ggc cag cga      245
Trp Thr Val Leu Ile Leu Phe Ser Cys Cys Cys Ala Phe Arg His Arg
60                65                70

aga gct aac ctg agg ctg cca cca cag cag cgg cag cgt gaa atc aac      293
Arg Ala Lys Leu Arg Leu Gln Gln Gln Arg Gln Arg Glu Ile Asn
75                80                85

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Leu Leu Ala Tyr His Gly Ala Cys His Gly Ala Gly Pro Phe Pro Thr
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Gly Ser Leu Leu Asp Leu Arg Phe Leu Ser Thr Phe Lys Pro Pro Ala
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tac gag gat gtg gtt cag cgc cca ggc aca cca cca cct tat act      437
Tyr Glu Asp Val Val His Arg Pro Gly Thr Pro Pro Pro Tyr Thr
125                130                135

gtg gcc cca ggc cgc ccc ttg act gct tcc agt gaa caa acc tgc tgt      485
Val Ala Pro Gly Arg Pro Leu Thr Ala Ser Ser Glu Gln Thr Cys Cys
140                145                150

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155                160                165

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Gly Val Ser Ser His Gln Ser Ala Pro Pro His Gln Gln Gly Glu Pro
170                175                180                185

ggg gca ggg gtg acc cct gcc tcc aca ccc ccc tcc tgc cgc tat cgc      629
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190                195                200

pgt tta act ggc gac tcc ggt att gag ctg tgc cct tgt cct gcc tcc      677
Arg Leu Thr Gly Asp Ser Gly Ile Glu Leu Cys Pro Cys Pro Ala Ser
205                210                215

pgt gag ggt gag cca gtc aag gag gtg agg gtt agt gcc acc ctg cca      725
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Asp Leu Glu Asp Tyr Ser Pro Cys Ala Leu Pro Pro Glu Ser Val Pro
235                240                245

cag atc ttt ccc atg ggg ctg tct tcc agt gaa ggg gac atc cca      818
Gln Ile Phe Pro Met Gly Leu Ser Ser Ser Ser Gly Asp Ile Pro
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Asp Cys Leu Arg Asp Trp Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile	
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Gln Gln Thr His Arg Leu Tyr Arg Leu Lys Leu Glu Gln Leu Thr Lys	
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Leu Gln Asn Asn Cys Thr Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu	
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Gln Gln Leu Ala Leu Ala Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala	
60 65 70	
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Glu Ala Glu Gly Ala Ala Gln Gln Leu Glu Asn Gln Met Lys Glu Arg	
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Gln Gly Leu Phe Phe Asp Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly	
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Tyr Leu Thr Ile Ile Leu Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu	
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Ser Arg Ile Lys Gly Trp Trp Val Phe His His Tyr Val Ser Thr Phe	
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Leu Ser Gly Val Met Leu Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys	
205 210 215	
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Phe Leu Gln Tyr Tyr Tyr Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala	
235 240 245 250	
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Leu Gly Glu Arg His Thr Met Asp Leu Thr Val Glu Gly Phe Gln Ser	
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Trp Met Trp Arg Gly Leu Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly	

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His Phe Trp Gln Leu Phe Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln			
285	290	295	
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Asp Pro Gln Cys Lys Glu Trp Gln Val Leu Met Cys Gly Phe Pro Phe			
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cac ctc ctt ttc ctc ggc aat ttc ttc acc acc ctg agg gtt gtg cac			1013
Leu Leu Leu Phe Leu Gly Asn Phe Phe Thr Thr Leu Arg Val Val His			
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His Lys Phe His Ser Gln Arg His Gly Ser Lys Lys Asp			
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Leu Leu Gln Leu Leu Val Leu Leu Leu Thr Leu Pro Leu His Leu Met			
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Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys Lys Ser Tyr Phe Pro Tyr			
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Leu Met Ala Val Leu Thr Pro Lys Ser Asn Arg Lys Met Glu Ser Lys			
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Lys Arg Gln Leu Phe Ser Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly			
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aaa gtg gcc cta ctg gag ctg ggc tgc gga acc gga gcc aac ttt cag			296
Lys Val Ala Leu Leu Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln			
	75 80 85		
ttc tac cca cgg gcc tgc agg gtc acc tgc cta gac cca aat ccc ccc			344
Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His			
	90 95 100		
ttt gag aag ttc ctg acc aag agc atg gct gag aac agg ccc ctc cca			392
Phe Gln Lys Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln			
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Tyr Gln Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala			
	120 125 130		
gat ggc tcc atg gat gtg gtg gtc tgc act ctg gtg ctg tgc tct gtg			488
Asp Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val			
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cag agc cca agg aag gtc ctg cag gag gtc cgg aga gta ctg aga cgg			536
Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg Pro			
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Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr Gly Ser	
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Trp Ala Phe Met Trp Gln Gln Val Phe Gln Pro Thr Trp Lys His Ile	
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gaa caa ttc tcc gaa atc caa atg gaa aga cag ccc ccc ccc ttg aag	64.6
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Trp Leu Pro Val Gly Pro His Ile Met Gly Lys Ala Val Lys	
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Ser Gly Ala His Gly Val Gln Val Tyr Leu Pro Gly Gln Gly Glu Val	

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Thr Ile Val Pro Arg Trp Met Arg Val Arg Arg	Ser Ser Glu Cys Met		
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gct caa gga gag ctc ttt ctg gat gat gga cac	agg ttc aac tat cag	639	
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Thr Arg Gln Glu Phe Leu Leu Arg Arg Phe Ser	Phe Ser Gly Asn Thr		
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 <12> DNA
 <13> Homo sapiens

<10>
 <11> CDS
 <222> (75)...(555)

<400> 30

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gactggcccg ca atg gac aag ctg aag aag gtg ctg agc ggg cag gac aag      111
Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr
1 5 10
gag aac cgg acc ggc ctg tcc gag gtt gtt gag gca tct tca tta agc      160
Glu Asp Arg Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser
15 20 25
agg agt acc agg ata aaa ggc ttc att cgg tgt ttt ggt ata gga att      200
Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile
30 35 40 45
tcc tgc tca ctg ctg ggt aat ggt ctg ctg tgg ggg ccc agg aag tga      250
Leu Cys Ser Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly
50 55 60
tca aac ctg ttc gca gtg ttt tat acc tct gtt aat acc gca tca att      300
Leu His Leu Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile
65 70 75
agg agt acc att ttc ctg atg gga cca gtc aac cag ctg aat cga atg      350
Gly Ser Thr Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met
80 85 90
tct gag cct acc cgt ttg att gca aat acc arg gtc ctg ttt ggt ttt      400
Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe
95 100 105
aca ttt acc ctg tgt tct ggc ttt tgg tgg ctt aac aag gga ttc gca      450
Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala
110 115 120
att ttc ttc tgc att ttg cag tct ttg gca ttg aag tgg tca agc att      500
Leu Ile Phe Cys Ile Leu Glu Ser Leu Ala Leu Thr Trp Tyr Ser Leu
125 130 135 140
aac ttc ata cca ttt gca agg gat ggt ctg aag aag tgt ttt ggc ctg      550
Ser Phe Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val
145 150 155
tct ttt gca caattccagg ccagttttat gaggctttag aaggccactt ggcagaaa      600
Lys Leu Ala
160
ctgtgggac agttttgtta ctattctga aaattctgtt ctaccagat ggcctttta      650
cttgccgca atgtgttgt ttgtatttga acatttgag gttactttt gaggcaacaa      700
tactttctg aaattgaatg tcaatagcac aggtatgaga gttggtttt tatctgttg      750
gttggaatt ctctcagta cctgtttct ctctgpatc tgtccacac aattccatg      800
cttataaac tatcagtaa cagcacataa gctttgggtg caagtgaat ccaggtggca      850
aaagtccgc ccatcagaga tcaagggagc aaactgaagg gacagagttt tgggttcac      900
ttgttttca gcaaggagc cctcactgt gtctgca'a gactgagtt aattctactc      1000
tggcatctga gaacaagtga ctctgtttta gacaagccc tggagagcct ggcacatggag      1050
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1104

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<10> 11

<11> 1445

<12> PRT

<13> Homo sapiens

<400> 11

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Pro Gly Ile Ile Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu
35 40 45
Leu Glu His Cys Pro Ser Glu Val Thr Val Lys Ala Glu Leu Leu Lys
50 55 60
Thr Ala Ser Asn Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe
65 70 75 80

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Glu Lys Gly Ser Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn
 85 90 95
 Ser Ala Asp Glu Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp
 100 105 110
 Glu Ile Leu Phe Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg
 115 120 125
 Ile Ser Val Phe Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln
 130 135 140
 Glu Val Lys Phe Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr
 145 150 155 160
 Lys Thr Ser Leu Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile
 165 170 175
 Gln Gln Trp Leu Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr
 180 185 190
 Phe Gln Leu Ser Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val
 195 200 205
 Gln Val Asn Asp Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Gln Tyr
 210 215 220
 Val Leu Pro Lys Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser
 225 230 235 240
 Met Asn Ser Lys His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr
 245 250 255
 Gly Lys Pro Val Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser
 260 265 270
 Phe Trp Gly Lys Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly
 275 280 285
 Ser Ala Asn Phe Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp
 290 295 300
 Ser Ser Asn Gly Leu Ser Gln Tyr Leu Asp Leu Ser Phe Phe Gly Pro
 305 310 315 320
 Val Glu Ile Leu Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg
 325 330 335
 Asn Val Ser Thr Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu
 340 345 350
 Phe Phe Asp Tyr Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala
 355 360 365
 Thr Val Lys Val Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu
 370 375 380
 Arg Arg Asn Asn Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu
 385 390 395 400
 Tyr Trp Ser Gly Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln
 405 410 415
 Lys Ile Asn Tyr Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Gln Phe
 420 425 430
 Pro Ile Leu Glu Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu
 435 440 445
 Gly Ser Lys Ser Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser
 450 455 460
 Lys Thr Tyr Ile Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly
 465 470 475 480
 Ser Pro Phe Glu Leu Val Val Ser Gly Asn Lys Arg Leu Lys Gln Leu
 485 490 495
 Ser Tyr Met Val Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln
 500 505 510
 Asn Ser Thr Met Phe Ser Leu Thr Pro Gln Asn Ser Trp Thr Pro Lys
 515 520 525
 Ala Cys Val Ile Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser
 530 535 540
 Asp Val Leu Lys Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys
 545 550 555 560
 Leu Tyr Trp Ser Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu

Arg	Ile	Ser	Val	Thr	Gln	Pro	Asp	Ser	Ile	Val	Gly	Ile	Val	Ala	Val	565	570	575
			580					585					590					
Asp	Lys	Ser	Val	Asn	Leu	Met	Asn	Ala	Ser	Asn	Asp	Ile	Thr	Met	Glu			
	595						600					605						
Asn	Val	Val	His	Glu	Leu	Glu	Leu	Tyr	Asn	Thr	Gly	Tyr	Tyr	Leu	Gly			
	610					615					620							
Met	Phe	Met	Asn	Ser	Phe	Ala	Val	Phe	Gln	Glu	Cys	Gly	Leu	Trp	Val			
	625				630					635					640			
Leu	Thr	Asp	Ala	Asn	Leu	Thr	Lys	Asp	Tyr	Ile	Asp	Gly	Val	Tyr	Asp			
			645					650					655					
Asn	Ala	Glu	Tyr	Ala	Glu	Arg	Phe	Met	Glu	Glu	Asn	Glu	Gly	His	Ile			
	660							665					670					
Val	Asp	Ile	His	Asp	Phe	Ser	Leu	Gly	Ser	Ser	Pro	His	Val	Arg	Lys			
	675						680					685						
His	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Leu	Asp	Thr	Asn	Met	Gly	Ser	Arg			
	690					695				700								
Ile	Tyr	Gln	Glu	Phe	Glu	Val	Thr	Val	Pro	Asp	Ser	Ile	Thr	Ser	Trp			
	705				710					715					720			
Val	Ala	Thr	Gly	Phe	Val	Ile	Ser	Glu	Asp	Leu	Gly	Leu	Gly	Leu	Thr			
			725					730					735					
Thr	Thr	Pro	Val	Glu	Leu	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Ile	Phe	Leu			
			740					745					750					
Asn	Leu	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Glu	Phe	Ala	Leu	Glu	Ile			
	755						760					765						
Thr	Ile	Phe	Asn	Tyr	Leu	Lys	Asp	Ala	Thr	Glu	Val	Lys	Val	Ile	Ile			
	770					775					780							
Glu	Lys	Ser	Asp	Lys	Phe	Asp	Ile	Leu	Met	Thr	Ser	Ser	Glu	Ile	Asn			
	785				790				795						800			
Ala	Thr	Gly	His	Gln	Gln	Thr	Leu	Leu	Val	Pro	Ser	Glu	Asp	Gly	Ala			
			805						810					815				
Thr	Val	Leu	Phe	Pro	Ile	Arg	Pro	Thr	His	Leu	Gly	Glu	Ile	Pro	Ile			
			820				825						830					
Thr	Val	Thr	Ala	Leu	Ser	Pro	Thr	Ala	Ser	Asp	Ala	Ile	Thr	Gln	Met			
	835						840						845					
Ile	Leu	Val	Lys	Ala	Glu	Gly	Ile	Glu	Lys	Ser	Tyr	Ser	Gln	Ser	Ile			
	850					855					860							
Leu	Leu	Asp	Leu	Thr	Asp	Asn	Arg	Leu	Gln	Ser	Thr	Leu	Lys	Thr	Leu			
	865				870				875						880			
Ser	Phe	Ser	Phe	Pro	Pro	Asn	Thr	Val	Thr	Gly	Ser	Glu	Arg	Val	Gln			
			885					890						895				
Ile	Thr	Ala	Ile	Gly	Asp	Val	Leu	Gly	Pro	Ser	Ile	Asn	Gly	Leu	Ala			
		900						905					910					
Ser	Leu	Ile	Arg	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile	Asn			
		915					920					925						
Phe	Ala	Pro	Asn	Ile	Tyr	Ile	Leu	Asp	Tyr	Leu	Thr	Lys	Lys	Lys	Gln			
	930					935					940							
Leu	Thr	Asp	Asn	Leu	Lys	Glu	Lys	Ala	Leu	Ser	Phe	Met	Arg	Gln	Gly			
	945				950					955					960			
Tyr	Gln	Arg	Glu	Leu	Leu	Tyr	Gln	Arg	Glu	Asp	Gly	Ser	Phe	Ser	Ala			
			965					970						975				
Phe	Gly	Asn	Tyr	Asp	Pro	Ser	Gly	Ser	Thr	Trp	Leu	Ser	Ala	Phe	Val			
		980					985						990					
Leu	Arg	Cys	Phe	Leu	Gln	Ala	Asp	Pro	Tyr	Ile	Asp	Ile	Asp	Gln	Asn			
		995					1000					1005						
Val	Leu	His	Arg	Thr	Tyr	Thr	Trp	Leu	Lys	Gly	His	Gln	Lys	Ser	Asn			
	1010					1015					1020							
Gly	Glu	Phe	Trp	Asp	Pro	Gly	Arg	Val	Ile	His	Ser	Glu	Leu	Gln	Gly			
	1025					1030				1035					1040			
Gly	Asn	Lys	Ser	Pro	Val	Thr	Leu	Thr	Ala	Tyr	Ile	Val	Thr	Ser	Leu			
			1045					1050						1055				

Leu Gly Tyr Arg Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile
 1060 1065 1070
 His Phe Leu Glu Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr
 1075 1080 1085
 Leu Ala Leu Ile Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala
 1090 1095 1100
 Lys Glu Ala Leu Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly
 1105 1110 1115 1120
 Met Gln Phe Trp Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln
 1125 1130 1135
 Pro Arg Ser Leu Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His
 1140 1145 1150
 Phe Leu Gln Phe Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu
 1155 1160 1165
 Ser Arg Gln Arg Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr
 1170 1175 1180
 Thr Val Ala Leu Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr
 1185 1190 1195 1200
 Glu Arg Thr Asn Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser
 1205 1210 1215
 Pro Val Lys Phe Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr
 1220 1225 1230
 Ala Glu Leu Ala Val Val Gln Pro Thr Ala Val Asn Ile Ser Ala Asn
 1235 1240 1245
 Gly Phe Gly Phe Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys
 1250 1255 1260
 Ala Ser Gly Ser Ser Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala
 1265 1270 1275 1280
 Phe Asp Leu Asp Val Ala Val Lys Gln Asn Lys Asp Asp Leu Asn His
 1285 1290 1295
 Val Asp Leu Asn Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly
 1300 1305 1310
 Met Ala Leu Met Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser
 1315 1320 1325
 Glu Ala Ile Ser Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His
 1330 1335 1340
 Gly Lys Leu Asn Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys
 1345 1350 1355 1360
 Val Asn Ile Pro Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp
 1365 1370 1375
 Ala Ser Val Ser Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val
 1380 1385 1390
 Arg Ser Tyr Asn Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser
 1395 1400 1405
 Asp Val Gln Gly Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His
 1410 1415 1420
 His His Ser Ser Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe
 1425 1430 1435 1440
 Met Glu Leu Trp Leu
 1445

0210 - 32
 0211 - 582
 0212 - PRT
 0213 - Homo sapiens

0400 - 32
 Met Phe Pro Ala Gly Pro Pro Ser His Ser Leu Leu Arg Leu Pro Leu
 1 5 10 15
 Leu Gln Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly
 20 25 30

Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
 45 45
 Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe
 50 50
 Val Arg Tyr His Tyr Asn Gly Thr Phe Glu Asp Gly Lys Lys Phe Asp
 55 55
 Ser Ser Tyr Asp Arg Asn Phe Leu Val Ala Ile Val Val Gly Val Gly
 60 60
 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
 65 65
 Glu Arg Arg Arg Ser Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
 70 70
 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Phe Leu Tyr Phe Asp Val
 75 75
 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Phe Val Gln Val Ser Thr
 80 80
 Ser Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
 85 85
 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
 90 90
 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
 95 95
 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
 100 100
 His Arg Arg Lys Ile Ile Ile Pro Pro Pro Leu Ala Tyr Gly Glu Lys
 105 105
 Lys Tyr Gly Thr Val Ile Pro Pro Gln Ala Ser Leu Val Phe His Val
 110 110
 Ser Leu Ile Asp Val His Asn Pro Lys Ala Ala Val Gln Ser Glu Thr
 115 115
 Ser Glu Leu Pro Pro Gly Cys Val Arg Arg Ala Gly Ala Gly Asp Phe
 120 120
 Met Arg Tyr His Tyr Asn Gly Ser Leu Met Asp Gly Thr Leu Phe Asp
 125 125
 Ser Ser Tyr Ser Arg Asn His Ile Tyr Asn Thr Tyr Ile Gly Gln Gly
 130 130
 Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu Gln Gly Ala Cys Met Gly
 135 135
 Glu Arg Arg Arg Ile Thr Ile Pro Pro His Leu Ala Tyr Gly Glu Asn
 140 140
 Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala Val Leu Ile Phe Asn Val
 145 145
 His Val Ile Arg Phe His Asn Pro Ala Asp Val Val Glu Ile Arg Thr
 150 150
 Leu Ser Arg Pro Ser Gln Thr Cys Asn Glu Thr Thr Lys Leu Gly Asp
 155 155
 Phe Val Arg Tyr His Tyr Asn Cys Ser Leu Leu Asp Gly Thr Glu Leu
 160 160
 Phe Thr Ser His Asp Tyr Gly Ala Pro Gln Glu Ala Thr Leu Gly Ala
 165 165
 Asn Lys Val Ile Glu Gly Leu Asp Thr Gly Leu Gln Gly Met Cys Val
 170 170
 Gly Glu Arg Arg Gln Leu Ile Val Pro Pro His Leu Ala His Gly Glu
 175 175
 Ser Gly Ala Arg Gly Val Pro Gly Ser Ala Val Leu Leu Phe Glu Val
 180 180
 Glu Leu Val Ser Arg Glu Asp Gly Leu Pro Thr Gly Tyr Leu Phe Val
 185 185
 Trp His Lys Asp Pro Pro Ala Asn Leu Phe Glu Asp Met Asp Leu Asn
 190 190
 Lys Asp Gly Glu Val Pro Pro Gln Glu Phe Ser Thr Phe Ile Lys Ala
 195 195

515	520	525
Gln Val Ser Glu Gly Lys	Gly Arg Leu Met Pro Gly Gln Asp Pro Glu	
530	535	540
Lys Thr Ile Gly Asp Met	Phe Gln Asn Gln Asp Arg Asn Gln Asp Gly	
545	550	555
Lys Ile Thr Val Asp Glu	Leu Lys Leu Lys Ser Asp Glu Asp Glu Glu	
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Arg Val His Glu Glu Leu		
580		

<210> 33
 <211> 410
 <212> PRT
 <213> Homo sapiens

<400> 33

Met Glu Leu Pro Ser Gly	Pro Gly Pro Glu Arg Leu Phe Asp Ser His
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20	30
Pro Val Gly Phe Cys Leu	Leu Val Leu Arg Leu Phe Leu Gly Ile His
40	45
Val Phe Leu Val Ser Cys	Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
50	60
Val Val Arg Thr Met Cys	Ala Val Leu Gly Leu Val Ala Arg Gln Glu
70	80
Asp Ser Gly Leu Arg Asp	His Ser Val Arg Val Leu Ile Ser Asn His
90	95
Val Thr Pro Phe Asp His	Asn Ile Val Asn Leu Leu Thr Thr Cys Ser
100	110
Thr Pro Leu Leu Asn Ser	Pro Pro Ser Phe Val Cys Trp Ser Arg Gly
120	125
Phe Met Glu Met Asn Gly	Arg Gly Glu Leu Val Glu Ser Leu Lys Arg
135	140
Phe Cys Ala Ser Thr Arg	Leu Pro Pro Thr Pro Leu Leu Leu Phe Pro
150	160
Glu Glu Glu Ala Thr Asn	Gly Arg Glu Gly Leu Leu Arg Phe Ser Ser
170	175
Trp Pro Phe Ser Leu Gln	Asp Val Val Gln Pro Leu Thr Leu Gln Val
180	190
Gln Arg Pro Leu Val Ser	Val Thr Val Ser Asp Ala Ser Trp Val Ser
200	205
Gln Leu Leu Trp Ser Leu	Phe Val Pro Phe Thr Val Tyr Gln Val Arg
215	220
Trp Leu Arg Pro Val His	Arg Gln Leu Gly Glu Ala Asn Glu Glu Phe
230	235
Ala Leu Arg Val Gln Gln	Leu Val Ala Lys Glu Leu Gly Gln Thr Gly
245	250
Thr Arg Leu Thr Pro Ala	Asp Lys Ala Glu His Met Lys Arg Gln Arg
260	270
His Pro Arg Leu Arg Pro	Gln Ser Ala Gln Ser Ser Phe Pro Pro Ser
280	285
Pro Gly Pro Ser Pro Asp	Val Gln Leu Ala Thr Leu Ala Gln Arg Val
290	300
Lys Glu Val Leu Pro His	Val Pro Leu Gly Val Ile Gln Arg Asp Leu
310	315
Ala Lys Thr Gly Cys Val	Asp Leu Thr Ile Thr Asn Leu Leu Glu Gly
325	330
Ala Val Ala Phe Met Pro	Glu Asp Ile Thr Lys Gly Thr Gln Ser Leu
340	345
Pro Thr Ala Ser Ala Ser	Lys Phe Pro Ser Ser Gly Pro Val Thr Pro

355	360	365
Gln Pro Thr Ala Leu Thr Phe	Ala Lys Ser Ser Trp	Ala Arg Gln Glu
370	375	380
Ser Leu Gln Glu Arg Lys Gln	Ala Leu Tyr Glu Tyr	Ala Arg Arg Arg
385	390	395
Phe Thr Glu Arg Arg Ala Gln	Glu Ala Asp	400
405	410	

<210> 34
 <211> 483
 <212> PRT
 <213> Homo sapiens

<400> 34

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Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg	
20 25 30	
Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro	
35 40 45	
Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp	
50 55 60	
Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Cys Ile	
65 70 75 80	
Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Lys Asp Tyr Lys	
85 90 95	
Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe Lys Gln Ser Ser	
100 105 110	
Cys Ser Tyr Asn Ile Glu Ser Tyr Trp Phe Tyr Glu Val Cys His Gly	
115 120 125	
Lys His Ile Asn Gln Tyr His Glu Glu Lys Glu Thr Gly Gln Lys Ile	
130 135 140	
Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala Lys Asn Leu Leu	
145 150 155 160	
Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys Ser Asn Glu Ile	
165 170 175	
Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr Tyr Pro Val Gly	
180 185 190	
Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn Arg Pro Arg Ser	
195 200 205	
Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys His Glu Ile Leu	
210 215 220	
Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val Val Ile Leu Thr	
225 230 235 240	
Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg Ala Ser Pro Val	
245 250 255	
Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro Phe Lys Pro Leu	
260 265 270	
Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu Arg Val Pro Phe	
275 280 285	
Arg Arg Asn Lys Glu Gln Asp Leu Gln Ser Thr Lys Glu Glu Arg Phe	
290 295 300	
Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln Pro Val Leu Thr	
305 310 315 320	
Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp Gln Leu Ile Lys	
325 330 335	
Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly Val Gly Trp Trp	
340 345 350	
Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln Tyr His Glu Asp	
355 360 365	
Lys Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr Trp Asn Gln Glu	

370	375	380
Glu His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg Ala Tyr His Leu		
385	390	395
Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser His Phe Tyr Gly		400
	405	410
Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg Gln Val Thr Val		415
	420	430
Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala Val Thr Val Tyr		440
	435	445
Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly Val Glu Ser Pro		450
	455	460
Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn Gly Leu Leu Ser		465
465	470	475
Leu Pro Asn		480

GI10: 35

GI11: 607

GI12: PRT

GI13: Homo sapiens

GI00: 35

Met Gly Phe Glu Glu Leu Leu Glu Gln Val Gly Gly Phe Gly Pro Phe		
1	10	15
Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro Arg Val Leu Leu Pro		
20	25	30
Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala Val Pro Ala His Arg		
35	40	45
Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser His Gln Asp Val Trp		
50	55	60
Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly Thr Leu Ser Ser Cys		
65	70	75
Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn Thr Thr Leu Gly Gln		
80	85	90
Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu Pro Ala Thr Val Pro		
100	105	110
Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu Phe Ser Ser Thr Ile		
115	120	125
Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile His Leu Glu Val Glu		
130	135	140
Cys Arg Trp Arg Gln Ser Pro Trp Glu Ala Ala Gly Arg Gly Leu Pro		
145	150	155
Trp Glu Glu Ala Glu Ala Ala Gly Leu Gly Arg Asp Lys Val Ser Tyr		
160	165	170
Ser Pro Ser Trp Arg Glu Ser Leu Gly Gly Leu Leu Ser Gly Met Glu		
175	180	185
Trp Asp Leu Val Cys Glu Gln Lys Gly Leu Asn Arg Ala Ala Ser Thr		
190	195	200
Phe Phe Phe Ala Gly Val Leu Val Gly Ala Val Ala Phe Gly Tyr Leu		
205	210	215
Ser Asp Arg Phe Gly Arg Arg Arg Leu Leu Leu Val Ala Tyr Val Ser		
220	225	230
Thr Leu Val Leu Gly Leu Ala Ser Ala Ala Ser Val Ser Tyr Val Met		
235	240	245
Phe Ala Ile Thr Arg Thr Leu Thr Gly Ser Ala Leu Ala Gly Phe Thr		
250	255	260
Ile Ile Val Met Pro Leu Glu Leu Glu Trp Leu Asp Val Glu His Arg		
265	270	275
Thr Val Ala Gly Val Leu Ser Ser Thr Phe Trp Thr Gly Gly Val Met		
280	285	290
Leu Leu Ala Leu Val Gly Tyr Leu Ile Arg Asp Trp Arg Trp Leu Leu		
295	300	

305	310	315	320
Leu Ala Val Thr	Leu Pro Cys Ala	Pro Gly Ile Leu Ser Leu Trp Trp	
	325	330	335
Val Pro Glu Ser	Ala Arg Trp Leu Leu Thr	Gln Gly His Val Lys Glu	
	340	345	350
Ala His Arg Tyr	Leu Leu His Cys Ala Arg Leu Asn Gly Arg Pro Val		
	355	360	365
Cys Glu Asp Ser	Phe Ser Gln Glu Ala Val Ser	Lys Val Ala Ala Gly	
	370	375	380
Glu Arg Val Val	Arg Arg Pro Ser Tyr Leu Asp Leu Phe Arg Thr Pro		
	385	390	395
Arg Leu Arg His	Ile Ser Leu Cys Cys Val Val Val Trp Phe Gly Val		
	405	410	415
Asn Phe Ser Tyr	Tyr Gly Leu Ser Leu Asp Val Ser Gly Leu Gly Leu		
	420	425	430
Asn Val Tyr Gln	Thr Gln Leu Leu Phe Gly Ala Val Glu Leu Pro Ser		
	435	440	445
Lys Leu Leu Val	Tyr Leu Ser Val Arg Tyr Ala Gly Arg Arg Leu Thr		
	450	455	460
Gln Ala Gly Thr	Leu Leu Gly Thr Ala Leu Ala Phe Gly Thr Arg Leu		
	465	470	475
Leu Val Ser Ser	Asp Met Lys Ser Trp Ser Thr Val Leu Ala Val Met		
	485	490	495
Gly Lys Ala Phe	Ser Gln Ala Ala Phe Thr Thr Ala Tyr Leu Phe Thr		
	500	505	510
Ser Glu Leu Tyr	Pro Thr Val Leu Arg Gln Thr Gly Met Gly Leu Thr		
	515	520	525
Ala Leu Val Gly	Arg Leu Gly Gly Ser Leu Ala Pro Leu Ala Ala Leu		
	530	535	540
Leu Asp Gly Val	Trp Leu Ser Leu Pro Lys Leu Thr Tyr Gly Gly Ile		
	545	550	555
Ala Leu Leu Ala	Ala Gly Thr Ala Leu Leu Leu Pro Glu Thr Arg Gln		
	565	570	575
Ala Gln Leu Pro	Glu Thr Ile Gln Asp Val Glu Arg Lys Ser Ala Pro		
	580	585	590
Thr Ser Leu Gln	Gln Glu Glu Met Pro Met Lys Gln Val Gln Asn		
	595	600	605

0210> 36
 0211> 314
 0212> ERT
 0213> Homo sapiens

0400> 36
Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala
1 10 15
Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser Gly Pro
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Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala
35 40 45
Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser
50 55 60
His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala
65 70 75 80
Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly Trp
85 90 95
Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser Leu
100 105 110
Gln Ala Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro
115 120 125
Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser

130 135 140
 Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln Ala
 145 150 155 160
 Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp
 165 170 175
 Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln
 180 185 190
 Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe
 195 200 205
 Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala
 210 215 220
 Gly Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 225 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val Val
 245 250 255
 Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr
 260 265 270
 Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln Ser
 275 280 285
 Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu Phe Phe Pro Leu
 290 295 300
 Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

<210> 37
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 37
 Met Glu Leu Ser Asp Val Thr Leu Ile Glu Gly Val Gly Asn Gln Val
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 Met Val Val Ala Gly Val Val Val Leu Ile Leu Ala Leu Val Leu Ala
 20 25 30
 Trp Leu Ser Thr Tyr Val Ala Asp Ser Gly Ser Asn Gln Leu Leu Gly
 35 40 45
 Ala Ile Val Ser Ala Gly Asp Thr Ser Val Leu His Leu Gly His Val
 50 55 60
 Asp His Leu Val Ala Gly Gln Gly Asn Pro Glu Pro Thr Glu Leu Pro
 65 70 75 80
 His Pro Ser Glu Ala Asn Thr Ser Leu Asp Lys Lys Ala Arg
 85 90

<210> 38
 <211> 218
 <212> PRT
 <213> Homo sapiens

<400> 38
 Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
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 Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
 20 25 30
 Ser Gln Leu Met Leu Tyr Ala Gln Arg Ala Glu Ala Arg Arg Lys Pro
 35 40 45
 Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
 50 55 60
 Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
 65 70 75 80
 Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
 85 90 95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
 100 105 110
 Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln Arg Cys Trp
 115 120 125
 Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala Val His Arg
 130 135 140
 Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu Leu Thr Ala
 145 150 155 160
 Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser Pro Arg Arg
 165 170 175
 Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His Pro Gly Pro
 180 185 190
 Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro Asp Pro Gly
 195 200 205
 Cys Thr Ala Ala Pro Cys His Ala Ala His
 210 215

<210> 39

<211> 460

<212> PRT

<213> Homo sapiens

<400> 39

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 Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn
 35 40 45
 Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr
 50 55 60
 Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln
 65 70 75 80
 Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu
 85 90 95
 Lys Glu Leu Arg Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu
 100 105 110
 Val Lys Asn Met Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu
 115 120 125
 Glu Glu Lys Ile Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln
 130 135 140
 Leu Thr Asn Leu Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu
 145 150 155 160
 Val Thr Ser Leu Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys
 165 170 175
 Asp Leu Leu Gln Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln
 180 185 190
 His Ser Gln Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile
 195 200 205
 Gln Glu Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg
 210 215 220
 Thr Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp
 225 230 235 240
 Gly Ile Pro Ala Gln Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr
 245 250 255
 Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val
 260 265 270
 Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg
 275 280 285
 Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr
 290 295 300

Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile
 305 310 315 320
 Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu
 325 330 335
 Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly
 340 345 350
 Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn
 355 360 365
 Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp
 370 375 380
 Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly
 385 390 395 400
 Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys
 405 410 415
 Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu
 420 425 430
 Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys
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 Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu
 450 455 460

<210> 40
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 40
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 Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr Leu Gly Gly Phe
 35 40 45
 Phe Ile Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu Trp Gly Leu Arg
 50 55 60
 Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly Pro Ser Gly Asn
 65 70 75 80
 Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr Glu Glu Ala Val
 85 90 95
 Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu Asp Gln Pro Pro
 100 105 110
 Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu Glu Glu Gln Pro
 115 120 125
 Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu Gln Arg Arg Met
 130 135 140
 Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro Gly Arg Ala Pro
 145 150 155 160
 Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser Thr Ala Pro Asp
 165 170 175
 Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro Leu Thr Pro Pro
 180 185 190
 Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp Asp Ser Val Phe
 195 200 205
 Tyr Glu Asp Asn Trp Ala Pro Pro
 210 215

<210> 41
 <211> 4335
 <212> DNA
 <213> Homo sapiens

<400> 41

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 <212> DNA
 <213> Homo sapiens

<400> 42						
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 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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 <212> DNA
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<210> 61

<211> 4473

<212> DNA

<213> Homo sapiens

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Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu Leu Glu His Cys
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cct tca cag gtg act gtg aag ggc gag ctg ctg aag aca gca tca aac 248
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Phe Lys Thr Leu Thr Pro Ser Leu Pro Leu Asn Ser Ala Asp Glu
85 90 95 100
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Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp Glu Ile Leu Phe
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215 220 225

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Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala Ser Leu Ile Arg			
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ccc agc tct ggc cgg gtg acc cct cag cca aca gcc cta aca ttt gcc 1216
Pro Ser Ser Gly Pro Val Thr Pro Gln Pro Thr Ala Leu Thr Phe Ala
360 365 370
aag tct tcc tgg gcc cgg cag gag agc ctg cag gag cgc aag caa gca 1264
Lys Ser Ser Trp Ala Arg Gln Glu Ser Leu Gln Glu Arg Lys Gln Ala
375 380 385
cta tat gaa tac gca aga agg aga ttc aca gag aga cga gcc cag gag 1312
Leu Tyr Glu Tyr Ala Arg Arg Arg Phe Thr Glu Arg Arg Ala Gln Glu
390 400 405
gct gar cgagctcaaa ggaacaggat ggcacacaga gcgcgaggac ggagactggg gg 1370
Ala Asp
410
gagccctcac ccaactcaca acagccttga tgggtgggtg gtaaaaaggg aaggatcagg 1430
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<210> 34

<211> 1652

<212> DNA

<213> Homo sapiens

<210>

<211> CDS

<212> (17)...(1468)

<400> 34

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1 5 10
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Pro Gly Gly Pro Val Leu Leu Val Leu Cys Gly Leu Glu Ala Ser
15 20 25
ggc gcc gcc cga gcc ctt cct caa ctc agc gat gac atc cct ttc cga 148
Gly Gly Gly Arg Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg
30 35 40
gtc aac tgg ccc ggc acc gag ttc tct ctg ccc aca act gga gtt tta 196
Val Asn Trp Pro Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu
45 50 55
tat aaa gaa gat aat tat gtc atc atg aca act gca cat aaa gaa aaa 244

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Tyr	Lys	Glu	Asp	Asn	Tyr	Val	Ile	Met	Thr	Thr	Ala	His	Lys	Glu	Lys	
				65					70					75		
tat	aaa	tgc	ata	ctt	ccc	ctt	gtc	aca	agt	ggg	gat	gag	gaa	gaa	gaa	292
Tyr	Lys	Cys	Ile	Leu	Pro	Leu	Val	Thr	Ser	Gly	Asp	Glu	Glu	Glu	Glu	
			80					85				90				
ang	gat	tat	aaa	ggc	ccc	aat	cca	aaa	gag	ctt	tgg	gag	cca	cca	ttt	340
Lys	Asp	Tyr	Lys	Gly	Pro	Asn	Pro	Arg	Glu	Leu	Leu	Glu	Pro	Leu	Pro	
			95				100					105				
aaa	caa	agc	agt	tgt	ccc	cac	aga	att	gag	ctt	tat	tgg	act	tac	gaa	388
Lys	Gln	Ser	Ser	Cys	Ser	Tyr	Arg	Ile	Glu	Ser	Tyr	Trp	Thr	Tyr	Gln	
	110					115					120					
gaa	tgt	cat	gga	aaa	ccc	att	ccc	cac	tac	cat	gaa	gag	aaa	gaa	act	436
Val	Cys	His	Gly	Lys	His	Ile	Arg	Gln	Tyr	His	Glu	Glu	Lys	Glu	Thr	
	125				130					135					140	
ggt	cag	aaa	ata	aat	att	cac	gag	tac	tac	ctt	ggg	aat	atg	tgg	gac	484
Gly	Gln	Lys	Ile	Asn	Ile	His	Glu	Tyr	Tyr	Leu	Gly	Asn	Met	Leu	Ala	
			145					150						155		
aag	aac	ctt	cta	ttt	gaa	aaa	gaa	cca	gaa	gca	gaa	gaa	aag	gaa	aaa	532
Lys	Asn	Leu	Leu	Phe	Glu	Lys	Glu	Arg	Glu	Ala	Glu	Glu	Lys	Glu	Lys	
			160				165						170			
tca	aat	gag	att	ccc	act	aaa	aat	atc	gaa	ggc	cag	atg	aca	cca	tac	580
Ser	Asn	Gln	Ile	Pro	Thr	Lys	Asn	Ile	Glu	Gly	Gln	Met	Thr	Pro	Tyr	
	175						180					185				
tat	cat	gtg	gga	tgg	gga	aat	ggc	aca	ccc	tgt	agt	tgg	aaa	cag	aac	628
Tyr	Pro	Val	Gly	Met	Gly	Asn	Gly	Thr	Pro	Cys	Ser	Leu	Lys	Gln	Asn	
	190					195					200					
agg	ccc	aga	tca	agt	act	gtg	atg	tac	ata	tgt	cat	ccc	gaa	ccc	atg	676
Arg	Pro	Arg	Ser	Ser	Thr	Val	Met	Tyr	Ile	Cys	His	Pro	Glu	Ser	Lys	
	205					210					215				220	
cat	gaa	att	cca	cca	gaa	ggt	gaa	ggt	aca	act	ttt	gaa	tat	gaa	ggt	724
His	Glu	Ile	Leu	Ser	Val	Ala	Glu	Val	Thr	Thr	Cys	Glu	Tyr	Glu	Val	
			225					230						235		
gtc	att	tgg	aca	cca	ctc	tgg	tgc	agt	cat	ccc	aaa	tat	agg	ttc	aga	772
Val	Ile	Leu	Thr	Pro	Leu	Leu	Cys	Ser	His	Pro	Lys	Tyr	Arg	Phe	Arg	
		240					245						250			
gca	ttt	ccc	gtg	aat	gac	ata	ttt	ttt	caa	tca	cag	cca	gga	ttt	cca	820
Ala	Ser	Pro	Val	Asn	Asp	Ile	Phe	Cys	Gln	Ser	Leu	Pro	Gly	Ser	Pro	
		255				260						265				
ttt	aag	ccc	ctc	acc	ctg	agg	cag	ctg	gag	cag	cag	gaa	gaa	ata	cca	868
Phe	Lys	Pro	Leu	Thr	Leu	Arg	Gln	Leu	Glu	Gln	Gln	Glu	Glu	Ile	Leu	
	270					275					280					
agg	gtg	ccc	ttt	agg	aga	aat	aaa	gag	gaa	gat	tgg	caa	tca	act	aaa	916
Arg	Val	Pro	Phe	Arg	Arg	Asn	Lys	Glu	Glu	Asp	Leu	Gln	Ser	Thr	Lys	
	285			290						295					300	
gaa	gag	aga	ttt	cca	ggg	atc	ccc	aag	tgg	att	gat	att	ggc	ttt	cag	964
Glu	Glu	Arg	Phe	Pro	Ala	Ile	His	Lys	Ser	Ile	Ala	Ile	Gly	Ser	Gln	
			305						310					315		
cca	gtg	ctc	act	gtt	ggg	aca	acc	ccc	ata	ccc	aaa	tgg	aca	gat	gac	1012
Pro	Val	Leu	Thr	Val	Gly	Thr	Thr	His	Ile	Ser	Lys	Leu	Thr	Asp	Asp	
			320					325					330			
caa	ctc	ata	aaa	gag	ttt	ctt	agt	ggt	ttt	tac	tgc	ttt	cgt	ggg	ggt	1060
Gln	Leu	Ile	Lys	Glu	Phe	Leu	Ser	Gly	Ser	Tyr	Cys	Phe	Arg	Gly	Gly	
		335				340						345				
gtc	ggt	tgg	tgg	aaa	tat	gaa	ttc	tgc	tat	ggc	aaa	cat	gta	cat	caa	1108
Val	Gly	Trp	Trp	Lys	Tyr	Glu	Phe	Cys	Tyr	Gly	Lys	His	Val	His	Gln	
	350					355					360					
tac	cat	gag	gac	aag	gat	agt	ggg	aaa	acc	ttt	gtg	ggt	gtc	ggg	aca	1156
Tyr	His	Glu	Asp	Lys	Asp	Ser	Gly	Lys	Thr	Ser	Val	Val	Val	Gly	Thr	
	365				370					375					380	
tgg	aac	caa	gaa	gag	cat	att	gaa	tgg	ggt	aag	aag	aat	act	ggt	aga	1204
Trp	Asn	Gln	Glu	Glu	His	Ile	Glu	Trp	Ala	Lys	Lys	Asn	Thr	Ala	Arg	

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      385      390      395
get tat cat ctt caa gac gat ggt acc cag aca gtc agg atg gtg tca 1252
Ala Tyr His Leu Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser
      400      405      410
cat ttt tat gga aat gga gat att tgt gat ata act gac aaa cca aga 1300
His Phe Tyr Gly Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg
      415      420      425
cag gtg act gta aca cta aag tgc aaa gaa tca gat tca cct cat get 1348
Gln Val Thr Val Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala
      430      435      440
gtt act gta tat atg cta gag cct cag tcc tgt caa tat att ctt ggg 1396
Val Thr Val Tyr Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly
      445      450      455      460
gtt gaa tct cca gtg atc tgt aaa atc tta gat aca gca gat gaa aat 1444
Val Glu Ser Pro Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn
      465      470      475
gga ctt ctt tct ctc ccc aac taaagatat taaagttagg ggaaa 1490
Gly Leu Leu Ser Leu Pro Asn
      480
gaaaagatca ttgaaagtca ttgataatttc tgtcccactg tgtctcatta tagagttctc 1550
agccattgga cctcttctaa aggatgggat aaaaagacac tcaaacactt tgtgaataca 1610
tatgtgtata taagaggtta ttgataaaact ttgaggcag ac 1652

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 <222> (20)...(1843)

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      1      5      10
ggc ttt ggg ccc ttc caa ctg cgg aat gtg gaa ctg ctg gcc ctg ccc 100
Gly Phe Gly Pro Phe Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro
      15      20      25
aga gtg ctg cta cca ctg cac ttc ctc ctg ccc atc ttc ctg gct gcc 148
Arg Val Leu Leu Pro Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala
      30      35      40
gtg cct gcc cag aga tgt gcc ctg cag ggt gcc cct gcc aac ttc agc 196
Val Pro Ala His Arg Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser
      45      50      55
cat cag gat gtg tgg ctg gag gcc cat ctt ccc cgg gag cct gat ggc 244
His Gln Asp Val Trp Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly
      60      65      70      75
agg ctg agc tcc tgc ctg cgc ttt gcc tat ccc cag gct ctg ccc aac 292
Thr Leu Ser Ser Cys Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn
      80      85      90
acc acg ttg ggg gaa gaa agg cag agc cgt ggg gag ctg gag gat gaa 340
Thr Thr Leu Gly Glu Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu
      95      100      105
cct gcc aca gtg ccc tgc tct cag gcc tgg gag tac gac cac tca gaa 388
Pro Ala Thr Val Pro Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu
      110      115      120
ttc tcc tct acc att gca act gag tcc cag gtc ggt att tac ata atc 436
Phe Ser Ser Thr Ile Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile
      125      130      135
cat ctg gag gtg gaa tgt cgg ttt agg cag tct ccc ttt gag gca gaa 484

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His	Leu	Glu	Val	Glu	Cys	Arg	Trp	Arg	Gln	Ser	Pro	Trp	Glu	Ala	Ala		
140					145					150					155		
ggt	aga	ggc	ggt	cct	tgg	gaa	gaa	gct	gag	ggt	gca	gga	ctg	ggg	agg	532	
Gly	Arg	Gly	Leu	Pro	Trp	Glu	Glu	Ala	Glu	Ala	Ala	Gly	Leu	Gly	Arg		
				160					165					170			
gac	aaa	ggt	tcc	tat	tcc	cca	aga	tgg	ggt	gaa	tgg	tgg	gga	ggg	tta	580	
Asp	Lys	Val	Ser	Tyr	Ser	Pro	Ser	Trp	Arg	Glu	Ser	Leu	Gly	Gly	Leu		
			175					180					185				
tta	tct	agt	atg	gag	tgg	tat	tgg	gtg	tgt	gag	cag	aaa	ggt	ctg	aac	628	
Leu	Ser	Gly	Met	Glu	Trp	Asp	Leu	Val	Cys	Glu	Glu	Lys	Gly	Leu	Asn		
			190				195					200					
aga	ggt	ggt	tcc	act	tta	tta	tta	gac	ggt	gca	ctg	tta	gga	ggt	gtg	676	
Arg	Ala	Ala	Ser	Thr	Phe	Phe	Phe	Ala	Gly	Val	Leu	Val	Gly	Ala	Val		
	205				210						215						
gac	tta	gga	tat	tgg	tcc	gac	agg	tta	gca	gga	agg	ggt	ctg	ctg	ctg	724	
Ala	Phe	Gly	Tyr	Leu	Ser	Asp	Arg	Phe	Gly	Arg	Arg	Arg	Leu	Leu	Leu		
	220			225					230				235				
gta	gac	tac	tgg	agt	acc	tgg	gtg	ctg	gta	ctg	gca	tat	gca	ggt	tcc	760	
Val	Ala	Tyr	Val	Ser	Thr	Leu	Val	Leu	Gly	Leu	Ala	Ser	Ala	Ala	Ser		
			240					245				250					
gtc	aga	tat	tta	gtg	tta	acc	ata	ata	gca	acc	ggt	act	ggt	tca	acc	800	
Val	Ser	Tyr	Val	Met	Phe	Ala	Ile	Thr	Arg	Thr	Leu	Thr	Gly	Ser	Ala		
			255				260					265					
ata	ggt	agt	tta	acc	ata	ata	tgg	atg	gca	ctg	gag	ctg	tat	tgg	ctg	860	
Leu	Ala	Gly	Phe	Thr	Ile	Ile	Val	Met	Pro	Leu	Glu	Leu	Glu	Trp	Leu		
			270				275					280					
ggt	tgg	ggt	gac	gga	acc	tgg	ggt	gta	gta	gta	aga	acc	acc	ctg	agg	916	
Asp	Val	Glu	His	Arg	Thr	Val	Ala	Gly	Val	Leu	Ser	Ser	Thr	Pro	Trp		
			285			290					295						
gca	ggt	ggt	gtg	ata	tgg	ctg	gca	ctg	gta	gga	tac	ctg	ata	ggt	gac	964	
Thr	Gly	Gly	Val	Met	Leu	Leu	Ala	Leu	Val	Gly	Tyr	Leu	Ile	Arg	Asp		
	300			305						310			315				
tgt	aga	ggt	ggt	gtg	cta	ggt	ata	acc	ggt	ggt	ggt	gca	gga	ggt	ata	1012	
Trp	Arg	Trp	Leu	Leu	Leu	Ala	Val	Thr	Leu	Pro	Cys	Ala	Pro	Gly	Ile		
			320						325				330				
ctg	aga	ctg	tgg	tgg	gtg	cct	tgg	tat	gca	gga	tgg	ggt	ctg	gca	gaa	1060	
Leu	Ser	Leu	Trp	Trp	Val	Pro	Glu	Ser	Ala	Arg	Trp	Leu	Leu	Thr	Glu		
			335				340					345					
ggt	tat	gta	aaa	gag	gca	gac	agg	tac	ctg	ctg	gac	tgt	gca	agg	ctg	1100	
Gly	His	Val	Lys	Glu	Ala	His	Arg	Tyr	Leu	Leu	His	Cys	Ala	Arg	Leu		
			350				355					360					
aat	ggt	ggg	cca	tcc	tat	gag	gac	acc	ctc	aga	cag	gag	ggt	gtg	agg	1156	
Asn	Gly	Arg	Pro	Val	Cys	Glu	Asp	Ser	Phe	Ser	Glu	Glu	Ala	Val	Ser		
			365				370					375					
taa	gtg	acc	gca	ggg	gaa	ggg	gtg	gtc	gta	ggt	acc	tta	tac	cta	gac	1204	
Lys	Val	Ala	Ala	Gly	Glu	Arg	Val	Val	Arg	Arg	Pro	Ser	Tyr	Leu	Asp		
	380			385							390						
ctc	tta	ggt	aca	aaa	ggg	ctc	gga	ctc	acc	tta	ctg	tgc	tgg	gtc	gtg	1252	
Leu	Phe	Arg	Thr	Pro	Arg	Leu	Arg	His	Ile	Ser	Leu	Cys	Cys	Val	Val		
			400						405				410				
gta	ggg	tta	gga	gtg	aac	ctc	tac	tat	tac	gga	ctg	acc	ctg	gat	gtg	1300	
Val	Trp	Phe	Gly	Val	Asn	Phe	Ser	Tyr	Tyr	Gly	Leu	Ser	Leu	Asp	Val		
			415				420					425					
tgg	ggg	ctg	ggg	gtg	aac	gtg	tac	gag	aaa	cag	ctg	tgg	tta	gga	ggt	1348	
Ser	Gly	Leu	Gly	Leu	Asn	Val	Tyr	Gln	Thr	Gln	Leu	Leu	Phe	Gly	Ala		
			430				435					440					
gtg	gaa	gtg	cca	tcc	atg	ctg	ctg	gtc	tac	tgg	tgg	gtg	cgc	tac	gca	1396	
Val	Glu	Leu	Pro	Ser	Lys	Leu	Leu	Val	Tyr	Leu	Ser	Val	Arg	Tyr	Ala		
	445					450					455						
gga	cgc	ggc	ctc	acg	caa	gcc	ggg	aca	ctg	ctg	ggc	acg	gcc	ctg	ggg	1444	
Gly	Arg	Arg	Leu	Thr	Gln	Ala	Gly	Thr	Leu	Leu	Gly	Thr	Ala	Leu	Ala		

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460          465          470          475
ttc ggc act aga ctg cta gtg tcc tct gat atg aag tcc tgg agc act    1492
Phe Gly Thr Arg Leu Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr
          480          485          490
gtc ctg gca gtg atg ggg aaa gct ttt tct gaa gct gcc ttc acc act    1540
Val Leu Ala Val Met Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr
          495          500          505
gcc tac ctg ttc act tca gag ttg tac cct acg gtg ctg aga cag aca    1588
Ala Tyr Leu Phe Thr Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr
          510          515          520
ggg atg ggg ctg act gca ctg gtg ggc ggg ctg ggg ggc tct tgg gcc    1636
Gly Met Gly Leu Thr Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala
          525          530          535
aca ctg ggc gcc ttg ctg gat gga gtg tgg ctg tca ctg ccc aag ctt    1684
Pro Leu Ala Ala Leu Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu
          540          545          550          555
act tat ggg ggg atc gcc ctg ctg gct gcc ggc acc gcc ctg ctg ctg    1732
Thr Tyr Gly Gly Ile Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu
          560          565          570
aca gag acg agg cag gca cag ctg cca gag acc atc cag gac ttg gag    1780
Pro Glu Thr Arg Gln Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu
          575          580          585
aga aag agt gcc cca acc agt ctt cag gag gaa gag atg ccc atg aag    1828
Arg Lys Ser Ala Pro Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys
          590          595          600
tag gtc cag aac taagtgggag tggaggcagg ccttccacag aagctctgca    1880
His Val Gln Asp
          605
ttaggggttg ggagagcaga agggcaggac ctgcaactca ggttgaggagt atcgaaacct    1940
tggcctaggg ccggagttgc tggcagtaac cgtccctctt gctcatccat ccttgattat    2000
tgggtttcta ggaacagttg aattccacaga atgpagtggg ctgctgggca cccctctcac    2060
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(222> (33)...(977)

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ctg ctg ggc ctg ctg ctg gct ggg gct gga ctg agg aag cgg gag tgg    101
Leu Leu Ala Leu Leu Leu Ala Arg Ala Gly Leu Arg Lys Pro Glu Ser
          10          15          20
cag gag ggc ggc cgg tta tca gga cca tgc ggc cga cgg gtc atc acg    149
Gln Glu Ala Ala Pro Leu Ser Gly Pro Cys Gly Arg Arg Val Ile Thr
          25          30          35
tcg cgc atc gtg ggt gga gag gac gcc gaa ctg ggg cgt tgg ccg tgg    197
Ser Arg Ile Val Gly Gly Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp
          40          45          50          55
cag ggg agc ctg cgc ctg tgg gat tcc cac gta tgc gga gtg agc ctg    245
Gln Gly Ser Leu Arg Leu Trp Asp Ser His Val Cys Gly Val Ser Leu
          60          65          70
ctc agc cac cgc tgg gca ctg aag ggc ggc caa tgc ttt gaa acc tat    293
Leu Ser His Arg Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr
          75          80          85

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agt gac att agt gat ccc ccc ggg tgg atg gtc cag ttt ggc cag ctg      341
Ser Asp Leu Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu
          90                      95                      100

act tcc atg cca tcc ttc tgg agc ctg cag gcc tac tac acc cgt tac      389
Thr Ser Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr
          105                      110                      115

ttc gta tgc aat atc tat ctg agc cct cgc tac ctg ggg aat tca ccc      437
Phe Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
          120                      125                      130

tat gac att gcc ttg gtg aac ctg tct gca cct gtc acc tac aat aaa      485
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr Lys
          140                      145                      150

cac atc cag ccc atc tgt ctg cag gcc tcc aca ttt gag ttt gag aac      533
His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Gln Phe Gln Asn
          155                      160                      165

cgg aca gac tgc tgg gtg aat ggc tgg ggg tac atc aaa gag gat gag      581
Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys Gln Asp Gln
          170                      175                      180

gca ctg cca tct ccc cac acc ctg cag gaa gtt cag gtc gcc atc ata      629
Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln Val Ala Ile Ile
          185                      190                      195

aac aac tct atg tgc aac cac ctg ttc ctg aag tac agt ttc cgc aag      677
Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys Tyr Ser Phe Arg Lys
          200                      205                      210

gac atc ttc gga gac atg gtt tgt gct ggc aat gcc caa ggc ggg aag      725
Asp Ile Phe Gly Asp Met Val Cys Ala Gly Asn Ala Gln Gly Gly Lys
          220                      225                      230

gat gca tgc ttc ggt gac tca ggt gga ccc ttg gcc tgt aac aag aat      773
Asp Ala Cys Phe Gly Asp Ser Gly Gly Pro Leu Ala Cys Asn Lys Asn
          235                      240                      245

gga ctg tgg tat cag att gga gtc gtg agc tgg gga gtg gcc tgt ggt      821
Gly Leu Trp Tyr Gln Ile Gly Val Val Ser Trp Gly Val Gly Cys Gly
          250                      255                      260

cgg tcc aat cgg ccc ggt gtc tac acc aat atc agc cac cac ttt gag      869
Arg Pro Asn Arg Pro Gly Val Tyr Thr Asn Ile Ser His His Phe Gln
          265                      270                      275

tgg atc cag aag ctg atg gcc cag agt ggc atg tcc cag cca gac ccc      917
Trp Ile Gln Lys Leu Met Ala Gln Ser Gly Met Ser Gln Pro Asp Pro
          280                      285                      290

tcc tgg ccg cta ctg ttt ttc cct ctt ctg tgg gct ctg cca ctg ctg      965
Ser Trp Pro Leu Leu Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu
          300                      305                      310

ggg ccg gtc tgagcctacc tgagcccatg cagcctgggg ccactgccaa gtcagg      1020
Gly Pro Val

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ccctggttct cttctgtctt gtttggtaat aaacacattc cagttgatgc ctgacagggc      1080
attcttc                                     1087

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<210> 57
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gccgggacaa ctggtcttat caggagggt ggggcaggc agccttcgg ttcggttggg      120
cccatggacc ccagtcacac gccgaggga taggaacac caaagcgga accttcgct      180

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cagaaaaagg cgtggaccct gccagcagcc aggcc atg gag ctc tct gat gtc 233
Met Glu Leu Ser Asp Val
1 5
acc cta att gag ggt gtg ggt aat gag gtg atg gtg gtg gca ggt gtg 281
Thr Leu Ile Glu Gly Val Gly Asn Glu Val Met Val Val Ala Gly Val
10 15 20
gtg gtg ctg att cta gcc ttg gtc cta gct tgg ctc tct acc tac gta 329
Val Val Leu Ile Leu Ala Leu Val Leu Ala Trp Leu Ser Thr Tyr Val
25 30 35
gca gag agc ggt agc aac cag ctc ctg ggc gct att gtg tca gca ggc 377
Ala Asp Ser Gly Ser Asn Gln Leu Leu Gly Ala Ile Val Ser Ala Gly
40 45 50
gac aca tcc gtc ctc cac ctg ggg cat gtg gac cac ctg gtg gca ggc 425
Asp Thr Ser Val Leu His Leu Gly His Val Asp His Leu Val Ala Gly
55 60 65 70
caa ggc aac ccc gag cca act gaa ctc ccc cat cca tca gag gca aat 473
Gln Gly Asn Pro Glu Pro Thr Glu Leu Pro His Pro Ser Glu Ala Asn
75 80 85
act tcc ctg gac aag aaa gcc aga tgaactgat ctaccagggc cgc 520
Thr Ser Leu Asp Lys Lys Ala Arg
90
ctgctacaag acccagcccg cacactgggt tctctgaaca ttaccgacaa ctgtgtgatt 580
cactgcaccc gctcacccccc agggtcaggt gtctcagggc cctcagccctc ctgtggccccc 640
tcgggcactg agccacccag ccttgggtgtc aatgtgggga ggcctcatggt ggcctgtcttc 700
gtgggtgtgt tgggtgtggt ctggtaattc cgaatcaatt accgcccaatt ctccacagca 760
cctggcactc tctccctggt gggagtcacc gtctctctca gcttcttagt atttgggatg 820
tatggagcat aaggacatag caagaaaatg aaaggccatg tctttctctt ttatggccctc 880
ccaacttttc ctggcccaag ctgggcccba gggccgggga gggagggggtg gaaaggatgt 940
gatggaaatc tcttcctatg gacacaggag gcaagtatgc ggcctccctt tctcatccac 1000
aggagtacac atgtccctcc cgtgagagca caactcaggt agaaatgagg atgtcatctt 1060
cctcactttc tagggtcttc tgaaggagtt caaagctgtt ggcacaagtc agtgggggagc 1120
ctgggtcttc agattccctc ccactgtgtg ttctgactct tcccagtgtc ctgcatgtct 1180
gcccccagca ccaggggtgt cctgcaaggg cagctcagca tggcccccagc acacctccgt 1240
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acactggcgg gaatgaagat tgtggccagc ttctcttatg ggcaccttagc cgccttcacc 1360
tcttctctt acccttttag aggaataggg tgtctctcct tctttcaaaag cacttttgtt 1420
gcattttatt ttattttttt aagagtccct catagagctc agtcagggaag gggatggggc 1480
accagccaa gcccccagca ttgggagcgg ccaggccaca gctgtgtctc cagtatgctt 1540
caggtgttaa gcaagagaca gcaatggccc ttggccagcg tctacccctg ccccaactcca 1600
aggactgggt atggattgtt gggccctagg ctcttgcttc tggggctatt ggagggtcag 1660
tgtctgtgac tgaataaaat tccattttgt gggtc 1694

<210> 58
<211> 1522
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (12)...(668)

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Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln
1 5 10
ctg atc atg cag ttg ggt tgg gtg ctg ctc asa cgc tgc ccc ttt tgg 98
Leu Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp
15 20 25
ggc tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc 146
Gly Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg
30 35 40 45

cgg aag ccc gac atc cca gtc cct tac ctg tat ttc gac atg ggg gca 194
 Arg Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala
 50 55 60
 gcc gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg 242
 Ala Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp
 65 70 75
 ttc ggc ctg ggg gcc gca ctc caa tgg gcc att agc acc tac gcc gcc 290
 Phe Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala
 80 85 90
 tac atc ggc gcc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg 338
 Tyr Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met
 95 100 105
 tac tgc cgc acc gct gcc atc atc ggc gga ctt tct tgt gtt gcc sag 386
 Tyr Ser Arg Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln
 110 115 120 125
 cgg tgc tgc gga gct gta cgg cgg gaa acc tgc cag cgc ctc cct gca 434
 Arg Cys Trp Gly Ala Val Pro Pro Gln Thr Ser Gln Pro Leu Pro Ala
 130 135 140
 gtc cac cgg cca ggt gtt cct ggg tat cta cct cat ctg tgt gcc cta 482
 Val His Arg Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu
 145 150 155
 ctc act gca gca cag caa gga gga cgg gct ggc gta tct gaa cca tct 530
 Leu Thr Ala Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Gln Pro Ser
 160 165 170
 ccc agg agg gga gct gat gat cca gct gtt ctt cgt gct gta tgg cat 578
 Pro Arg Arg Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His
 175 180 185
 ctt ggc cct gga ctt tct gtc agg cta cta cgt gac cct tgc tgc cca 626
 Pro Gly Pro Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro
 190 195 200 205
 gat cct gcc tgt act gct gcc ccc tgt cat gct gct cat tcatg 670
 Asp Pro Gly Cys Thr Ala Ala Pro Cys His Ala Ala His
 210 215
 gcaatgttgc tcaatggcac aacacggggc gtgttgagtt ctggaaccag atgaagctcc 730
 tgggagagag tgggggcacc ttgggaactg ctgtcatctg gccactgatg gctgagtttt 790
 atggcaagag gctgagatgg gcaacaggag ccaactgagg tcacactgcc ttctctcttg 850
 ctggccacgc tgggttttat ttaatgcttt tggctctgtt gtttgatctt ttgctctctt 910
 aaaaatgttt ttggagttta agaggcagct catttctcca aattctctggg ctccagcgctt 970
 gggagggcag gacccctggc actaatgctg cacagttttt ttctctgtta ggagagctga 1030
 ggccagctgc ccaatgagtc tccctgtcct gagaaaggag tatggcaggg ctgggatgcg 1090
 gctactgaga gtgggagagt gggagacaga ggaagggaaga tggagattgg aagtgagcaa 1150
 atgtgaaaaa ttctctcttg aacctggcag atgcaactag gctctgcagt gctgtttgga 1210
 gacttgaga gggagtgctg gtgttgacac atgtgpatca ggccnaggaa gggcacaggg 1270
 gctgagcaat acagaagtca catgggttct cagggtatgc caggggcaga aacagtaccg 1330
 gctctctgtc actcactttg agagttagag agacactgtt ctgctctggg ctgtgaaggg 1390
 gtggagcagg cagtggcag ctttgcctt cctgctgtct ctgtttctag ctccatggtt 1450
 ggcttggtgg gggtgagtt ccttcccaaa caccagacca cacagtctc caaaaataaa 1510
 cattttatat ag 1522

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 <211> 1591
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (44)...(1426)

<400> 59
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 Met Phe Thr Ile

1

aag ctc ctt ctt ttt att gtt cct cta gtt att tcc tcc aga att gat	103
Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser Ser Arg Ile Asp	
5 10 15 20	
caa gac aat tca tca ttt gat tct cta tct cca gag cca aaa tca aga	151
Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu Pro Lys Ser Arg	
25 30 35	
ttt gct atg tta gac gat gta aaa att tta gcc aat ggc ctc ctt cag	199
Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn Gly Leu Leu Gln	
40 45 50	
ttg gga cat ggt ctt aaa gac ttt gtc cat aag acg aag ggc caa att	247
Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr Lys Gly Gln Ile	
55 60 65	
aat gac ata ttt caa aaa ctc aac ata ttt gat cag tct ttt tat gat	295
Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln Ser Phe Tyr Asp	
70 75 80	
cta tgg ctg caa acc agt gaa atc aaa gaa gaa gaa aag gaa ctg aga	343
Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu Lys Glu Leu Arg	
85 90 95 100	
aga act aca tat aaa cta caa gtc aaa aat gaa gag gta aag aat atg	391
Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met	
105 110 115	
tca ctt gaa ctc aac tca aaa ctt gaa agc ctc cta gaa gaa aaa att	439
Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile	
120 125 130	
cta ctt caa caa aaa gtg aaa tat tta gaa gag caa cta act aac tta	487
Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu	
135 140 145	
att caa aat caa cct gaa aat cca gaa cac cca gaa gta act tca ctt	535
Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu	
150 155 160	
aaa act ttt gta gaa aaa caa gat aat agc atc aaa gac ctt ctc cag	583
Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln	
165 170 175 180	
acc gtg gaa gac caa tat aaa caa tta aac caa cag cat agt caa ata	631
Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln Ile	
185 190 195	
aaa gaa ata gaa aat cag ctc aga agg act agt att caa gaa ccc aca	679
Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu Pro Thr	
200 205 210	
gaa att tct cta tct tcc aag cca aga gca cca aga act act ccc ttt	727
Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr Thr Pro Phe	
215 220 225	
ctt cag ttg aat gaa ata aga aat gta aaa cat gat ggc att cct gct	775
Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp Gly Ile Pro Ala	
230 235 240	
gaa tgt acc acc att tat aac aga ggt gaa cat aca agt ggc atg tat	823
Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr Ser Gly Met Tyr	
245 250 255 260	
gcc atc aga ccc agc aac tct caa gtt ttt cat gtc tac tgt gat gtt	871
Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val Tyr Cys Asp Val	
265 270 275	
ata tca ggt agt cca tgg aca tta att caa cat cga ata gat gga tca	919
Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg Ile Asp Gly Ser	
280 285 290	
caa aac ttc aat gaa acg tgg gag aac tac aaa tat ggt ttt ggg agg	967
Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr Gly Phe Gly Arg	
295 300 305	
ctt gat gga gaa ttt tgg ttg ggc cta gag aag ata tac tcc ata gtg	1015
Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile Tyr Ser Ile Val	
310 315 320	

aag caa tct aat tat gtt cta cga att gag ctg gaa gac tgg aaa gac 1063
Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp
325 330 335 340
aac aaa cat tat att gaa tat tct ttt tac ttg gga aat cac gaa acc 1111
Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr
345 350 355
aac tat aag cta cat cta gtt gag att act ggc aat gtc ccc aat gca 1159
Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala
360 365 370
atc cag gaa aac aaa gat ttg gtg ttt tct act tgg gat cac aaa gca 1207
Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala
375 380 385
aaa gga cac ttc aac tgt cca gag ggt tat tca gga ggc tgg tgg tgg 1255
Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp
390 395 400
cat tat gag tgt gga gaa aac aac cta aat ggt aaa tat aac aaa cca 1303
His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro
405 410 415 420
aga gca aaa tct aag cta gag agg aga aga gga tta tct tgg aag tct 1351
Arg Ala Lys Ser Lys Pro Glu Arg Arg Gly Leu Ser Trp Lys Ser
425 430 435
caa aat gga agg tta ttc tct ata aaa tca acc aaa atg ttg atc cat 1399
Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu Ile His
440 445 450
cca aca gat tca gaa agc ttt gaa tgaactgagg caaattttaa aggcgat 1450
Pro Thr Asp Ser Glu Ser Phe Glu
455 460
aatttaaca ttaactcat tccaggttaa tatgggtctaa taatctggga tttaattctt 1510
aagagaaagc ttgagaaata gattttttt tatctttaaag tcaactgtctt ttttaagitta 1570
aacatataat cacataacct t 1591

<210> 60

<211> 1249

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (134)...(784)

<400> 60

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ctccacctgg agcatgggt aacacgggag gaaaggaaaa gacagagtoa gacagggagc 120
ctggggagggg gcc atg gtr cca atg cac tta ctg ggg aga ctg gag aay 169
Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys
1 5 10
cag att ctc ctc ctg ttc tgc gcc tcc ttc cta ctg ggg ctg gct ttg 217
Pro Leu Leu Leu Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu
15 20 25
ctg ggc ata aag acg gac atc acc ccc gtt gct tat ttc ttt ctc aca 265
Leu Gly Ile Lys Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr
30 35 40
ttg ggt ggc ttc ttc ttg ttt gcc tat ctc ctg gtc cgg ttt ctg gaa 313
Leu Gly Gly Phe Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu
45 50 55 60
tgg ggg ctc cgg tcc cag ctc caa tca atg cag act gag agc cca ggg 361
Trp Gly Leu Arg Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly
65 70 75
ccc tca ggc aat gca cgg gac aat gaa gcc ttt gaa gtg cca ctc tat 409
Pro Ser Gly Asn Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr
80 85 90

gaa gag gcc gtg gtg gga cca gaa tcc cag tgc cgc ccc caa gag ttg	457
Glu Glu Ala Val Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu	
95 100 105	
gac caa cca ccc ccc taa ago act gtt gtg ata ccc cca gca cct gag	505
Asp Gln Pro Pro Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu	
110 115 120	
gag gaa caa cct agc cat cca gag ggg tcc agg aga gcc aaa ctg gaa	553
Glu Glu Gln Pro Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu	
125 130 135 140	
cag agg cga atg gcc tca gag ggg tcc atg gcc cag gaa gga agc cct	601
Gln Arg Arg Met Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro	
145 150 155	
gga aga gct cca atc aac ctt cgg ctt cgg gga cca cgg gct gtg tcc	649
Gly Arg Ala Pro Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser	
160 165 170	
act gct cca gat ctg cag ago ttg ggc cca gtc ccc aca tta gag cct	697
Thr Ala Pro Asp Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro	
175 180 185	
ctg act cca ccc cct gcc cat gat gtc tgc ttt ggt cag cct gat gat	745
Leu Thr Pro Pro Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp	
190 195 200	
gat agt gtt ttt tat gag gac aac tgg gca ccc cct taaatgact	790
Asp Ser Val Phe Tyr Glu Asp Asn Trp Ala Pro Pro	
205 210 215	
atccaaagat tttctctctc tccacacccag acctcgttcca tttagactaac atttttcagc	850
gactactatg tgtcagaacc aagtgtttct ggcctggacat cataaatggg gaettggacc	910
tcagagagag tcaggccacg gtaagccctt cccagctgag atctcgggtg cataacttga	970
ggttcctggg aacatttggg gacctacccc atatccaata ttccagcgt tagattgagg	1030
atgaggtagg gactgtatcc agagaaggcg gagaagggaag aagtaacctc tgagtggcgg	1090
ctatcgtctc tgttccaggc gcgtttccag ctgttagaac ccttaggett gacagctttg	1150
tgagttatta ttgaaaatg aggattccaa gaatccagagg agtttgataa tgcacagag	1210
ggacactgc tagtaantaa cattaataata attggaatg	1249

<210> 61

<211> 392

<212> PRT

<213> Homo sapiens

<400> 61

Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr Ala Gly Leu	
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Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu	
20 25 30	
Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys	
35 40 45	
Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys	
50 55 60	
Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly	
65 70 75 80	
Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His	
85 90 95	
Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln	
100 105 110	
Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln	
115 120 125	
Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly	
130 135 140	
Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met	
145 150 155 160	
Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys	
165 170 175	

His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys
 180 185 190
 Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val
 195 200 205
 Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala
 210 215 220
 Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe
 225 230 235 240
 Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly
 245 250 255
 Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg
 260 265 270
 Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Gln
 275 280 285
 Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly
 290 295 300
 Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu
 305 310 315 320
 Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly
 325 330 335
 Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
 340 345 350
 Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
 355 360 365
 Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg
 370 375 380
 Pro Arg Arg Ser Glu Lys Gln Pro
 385 390

<210> 62
 <211> 497
 <212> PRT
 <213> Homo sapiens

<400> 62
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 Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
 20 25 30
 Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
 35 40 45
 Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
 50 55 60
 Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
 65 70 75 80
 Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
 85 90 95
 Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
 100 105 110
 Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Trp Lys Gly Ala Ala
 115 120 125
 Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
 130 135 140
 Val Ala Ser Gln Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala
 145 150 155 160
 Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu
 165 170 175
 Leu Cys Gly Pro Val Gly Pro Arg Leu His Glu Leu Leu Asp Asp Asn
 180 185 190
 Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu
 195 200 205

Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro
 210 215 220
 His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met
 225 230 235 240
 Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp
 245 250 255
 Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu
 260 265 270
 Leu Gln Arg Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile
 275 280 285
 Pro Thr Gly Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg
 290 295 300
 Glu Leu Met Ser Ser Ile Val His Gln Gln Val Phe Pro Ala Val Thr
 305 310 315 320
 Ser Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala
 325 330 335
 Ser Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val
 340 345 350
 Gly Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg
 355 360 365
 Ser Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu
 370 375 380
 Val Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu
 385 390 395 400
 Ala Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala
 405 410 415
 Thr Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu
 420 425 430
 Phe Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro
 435 440 445
 Asn Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe
 450 455 460
 Thr Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly
 465 470 475 480
 Asp Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His
 485 490 495
 Tyr

0210> 63
 0211> 417
 0212> PRT
 0213> Homo sapiens

0300> 63
 Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro Phe Pro
 1 5 10 15
 Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala Val Arg
 20 25 30
 Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val Ala His
 35 40 45
 Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu Ala Pro
 50 55 60
 Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Ala Leu Leu Gly
 65 70 75 80
 Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala Leu Cys
 85 90 95
 Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val Val Gly
 100 105 110
 Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro His Leu
 115 120 125
 Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala Leu Val

120	135	140
Asn Val Gln Ile Pro Leu Leu Gly Gln Leu Val Glu Val Val Ala		
115	130	135
Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser Gln Asn		
165	170	175
Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu Leu Thr		
180	185	190
Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Gln Arg Met Ala Val		
195	200	205
Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys Gln Pro		
210	215	220
Gln Gly Ala Gln Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala Asn Lys		
225	230	235
Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Gln Phe Lys		
240	245	250
Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys Thr Gln		
255	260	265
Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg Leu Thr		
270	275	280
Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly Thr Leu		
285	290	295
Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Gln Gln Ile		
300	305	310
Ala Arg Ala Met Gly Val Ala Asp Gln Ala Leu Gly Asn Val Arg Thr		
315	320	325
Val Arg Ala Phe Ala Met Gln Gln Arg Gln Gln Gln Arg Tyr Gly Ala		
330	335	340
Gln Leu Gln Ala Cys Arg Cys Arg Ala Gln Gln Leu Gly Arg Gly Ile		
345	350	355
Ala Leu Phe Gln Gly Ser Ser Asn Ile Ala Phe Asn Cys Met Val Leu		
360	365	370
Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln Leu Thr		
375	380	385
Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val Gln Arg		
390	395	400
Leu		

110 - 64
 111 - 649
 112 - PRT
 113 - Homo sapiens

100 - 64
Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly Ser His Gln Pro Ala
1
Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu Asp His Ile Leu Pro
10
Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu Val Val Gly Ser Val
30
Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly Asp Phe Val Phe Asp
50
Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala Gly Val Val Gly Arg
65
Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Ser Phe Leu Gly Tyr
85
Cys Lys Ala Phe Arg Glu Ser Asn Lys Gln Gly Ala His Ser Ser Thr
100
Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala Val Ala Met Leu Cys
115
Lys Gln Gln Gly Ile Thr Val Leu Gly Leu Asn Ala Val Phe Asp Ile
130

Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile Val Gln Lys Val Leu
 145 150 155 160
 His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met Leu Arg Asn Gly Gly
 165 170 175
 Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly Gly Ala Gly Met Leu
 180 185 190
 Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro Pro Ala Phe Thr Glu
 195 200 205
 Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met Leu Val Arg Ala Val
 210 215 220
 Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp Leu Leu Leu Cys Pro
 225 230 235 240
 Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys Ile Pro Leu Ile Lys
 245 250 255
 Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala Ala Leu Trp Phe Cys
 260 265 270
 Leu Ile Gly Leu Ile Cys Gln Ala Leu Cys Ser Glu Asp Gly His Lys
 275 280 285
 Arg Arg Ile Leu Thr Leu Gly Leu Gly Phe Leu Val Ile Pro Phe Leu
 290 295 300
 Pro Ala Ser Asn Leu Phe Phe Arg Val Gly Phe Val Val Ala Glu Arg
 305 310 315 320
 Val Leu Tyr Leu Pro Ser Ile Gly Tyr Cys Val Leu Leu Thr Phe Gly
 325 330 335
 Phe Gly Ala Leu Ser Lys His Thr Lys Lys Lys Lys Leu Ile Ala Ala
 340 345 350
 Val Val Leu Gly Ile Leu Phe Ile Asn Thr Leu Arg Cys Val Leu Arg
 355 360 365
 Ser Gly Glu Trp Arg Ser Glu Glu Gln Leu Phe Arg Ser Ala Leu Ser
 370 375 380
 Val Cys Pro Leu Asn Ala Lys Val His Tyr Asn Ile Gly Lys Asn Leu
 385 390 395 400
 Ala Asp Lys Gly Asn Gln Thr Ala Ala Ile Arg Tyr Tyr Arg Glu Ala
 405 410 415
 Val Arg Leu Asn Pro Lys Tyr Val His Ala Met Asn Asn Leu Gly Asn
 420 425 430
 Ile Leu Lys Glu Arg Asn Glu Leu Gln Gln Ala Glu Glu Leu Leu Ser
 435 440 445
 Leu Ala Val Gln Ile Gln Pro Asp Phe Ala Ala Ala Trp Met Asn Leu
 450 455 460
 Gly Ile Val Gln Asn Ser Leu Lys Arg Phe Glu Ala Ala Glu Gln Ser
 465 470 475 480
 Tyr Arg Thr Ala Ile Lys His Arg Arg Lys Tyr Pro Asp Cys Tyr Tyr
 485 490 495
 Asn Leu Gly Arg Leu Tyr Ala Asp Leu Asn Arg His Val Asp Ala Leu
 500 505 510
 Asn Ala Trp Arg Asn Ala Thr Val Leu Lys Pro Glu His Ser Leu Ala
 515 520 525
 Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr Gly Asn Leu Ala Gln
 530 535 540
 Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu Ile Pro Asn Asp His
 545 550 555 560
 Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly Lys Ser Gln Lys Tyr
 565 570 575
 Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile Lys Ala Asn Pro Asn
 580 585 590
 Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu Tyr His Arg Trp Gly
 595 600 605
 His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile Ser Leu Gln Leu Asp
 610 615 620
 Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly Leu Leu Arg Arg Lys

625 630 635 640
 Leu Glu Leu Met Gln Lys Lys Ala Val
 645

<210> 65
 <211> 93
 <212> PRT
 <213> Homo sapiens

1400: 65
 Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
 1 5 10 15
 Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
 20 25 30
 Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
 35 40 45
 Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
 50 55 60
 Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
 65 70 75 80
 Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
 85 90

<210> 66
 <211> 425
 <212> PRT
 <213> Homo sapiens

1400: 66
 Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
 1 5 10 15
 Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
 20 25 30
 Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
 35 40 45
 Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
 50 55 60
 Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His
 65 70 75 80
 His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala
 85 90 95
 Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe
 100 105 110
 Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe
 115 120 125
 Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val
 130 135 140
 Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr
 145 150 155 160
 Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe
 165 170 175
 Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln
 180 185 190
 Gly Leu Leu Leu Leu Leu Pro Pro Pro Ser Val Pro Thr Gly Glu
 195 200 205
 Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val
 210 215 220
 Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr
 225 230 235 240
 Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser
 245 250 255

Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly
 260 265 270
 Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu
 275 280 285
 Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala
 290 295 300
 Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly
 305 310 315 320
 Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu
 325 330 335
 Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val
 340 345 350
 Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr
 355 360 365
 Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala
 370 375 380
 Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala
 385 390 395 400
 Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg
 405 410 415
 Lys Asp Cys Ala Asp Pro Cys Asp Ser
 420 425

<10> 67
 <11> 149
 <12> PRT
 <13> Homo sapiens

<100> 67
 Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
 1 5 10 15
 Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
 20 25 30
 Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
 35 40 45
 Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
 50 55 60
 Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 65 70 75 80
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
 85 90 95
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile
 100 105 110
 Pro Lys Leu Asn Arg Phe Leu Leu Phe Ile Gly Phe Val Cys Val
 115 120 125
 Leu Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro
 130 135 140
 Gly Tyr Leu Met Gly
 145

<10> 68
 <11> 396
 <12> PRT
 <13> Homo sapiens

<100> 68
 Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu
 1 5 10 15
 Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala
 20 25 30
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln

35	40	45
Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr		
50	55	60
Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu		
65	70	75
Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Gln Trp		
85	90	95
Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Gln		
100	105	110
Val Val Phe Ile Leu Gly Asp Ile Phe Asp Gln Gly Lys Trp Ser Thr		
115	120	125
Pro Gln Ala Trp Ala Asp Asp Val Gln Arg Phe Gln Lys Met Phe Arg		
130	135	140
His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile		
145	150	155
Gly Phe His Tyr His Met Asn Thr Tyr Lys Val Gln Arg Phe Gln Lys		
160	165	170
Val Phe Ser Ser Gln Arg Leu Phe Ser Trp Lys Gln Ile Asn Phe Val		
175	180	185
Met Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser		
190	195	200
Glu Thr Glu Ala His Leu Ile Gln Val Ser His Arg Leu Asn Cys Ser		
205	210	215
Arg Gln Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro		
220	225	230
Thr Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser		
235	240	245
Asp Ala Asn Cys Ser Gly Gln Asp Ala Ala Pro Ala Leu Gln Arg Asp		
250	255	260
Ile Pro Phe Lys Gln Asn Tyr Asp Val Leu Ser Arg Gln Ala Ser Gln		
265	270	275
Lys Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr		
280	285	290
His Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Gln Leu Ser		
295	300	305
Val Pro Ser Phe Ser Trp Arg Asn Arg Asn Pro Ser Phe Ile Met		
310	315	320
Gly Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro		
325	330	335
Arg Gln Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu		
340	345	350
Val Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu		
355	360	365
Ser Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg		
370	375	380

GI10 - 69
 GI11 - 650
 GI12 - PERT
 GI13 - Homo sapiens

GI400 - 69

Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Gln Leu Ser Glu Glu
1
Leu Val Gln Val Val Glu Asn Ser Gln Leu Ala Asp Gln Gln Asp Lys
10
Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly Leu Asp Ser
15
Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys Leu Lys Asn
50
Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu Met Ala Val

65	70	75	80
Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg Glu Lys Leu			
	85	90	95
Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp Arg Tyr Asp			
	100	105	110
Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu Leu Ser Cys			
	115	120	125
Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro Gly Gln Pro			
	130	135	140
Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr Asp Pro Phe			
	145	150	155
Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly Pro Arg Gln			
	165	170	175
Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu Asn Lys Ser			
	180	185	190
Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser Ser Phe Gln			
	195	200	205
Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln Ala Cys Glu			
	210	215	220
Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg Thr Trp Val			
	225	230	235
Lys Met Ser Leu Val Lys Thr Lys Glu Gln Asp Gly Arg Gln Ala Val			
	245	250	255
Glu Phe Arg Gln Glu Thr Ser Val Val Asn Tyr Ile Asp Gln Arg Pro			
	260	265	270
Ala Ala Lys Lys Ser Ala Gln Leu Phe Phe Val Val Phe Gln Trp Lys			
	275	280	285
Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala Asn Pro Trp			
	290	295	300
Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu Phe Lys Ala			
	305	310	315
Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys Ile Arg Lys			
	325	330	335
Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile Ser			
	340	345	350

<10> 70
 <11> 183
 <12> PET
 <13> Homo sapiens

1000> 70
Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Leu Ala Phe Ser Ala
1
5
10
Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln Val Pro
15
20
25
Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr His Arg
30
35
40
45
Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly Ala Leu
50
55
60
Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp Ala Pro
65
70
75
80
Pro Val Ala Arg Gly Ser Pro Ala Arg Phe Pro Gly Phe Arg Pro
85
90
95
Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr Ser Gly
100
105
110
Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met Leu Glu
115
120
125
Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu Thr Val
130
135
140
Phe Pro Ser Pro Ser Pro Gly Cys Asp

145

150

<210> 71
 <211> 1176
 <212> DNA
 <213> Homo sapiens

<400> 71

atggaggag	tgagcgcgc	gctggccgc	tgcacacgc	cggccctgg	cgccggcctg	60
gggtcagc	cgtgcgcgc	ggcgggcgc	ttgctctac	ggatcgccg	gaggatgaag	120
ccaaagcaca	cgatggcaca	ctgctgggtc	tgcacacgc	atacgttgt	gcctatggg	180
aaccgcacac	gctgggactg	tcacacactg	gaagagtaca	acggcttcca	ggagaacggc	240
gactacaaca	agccgacccc	cgcacagtag	ttggagcacc	tgaaccacgt	ggtgagcagg	300
ggccacagcc	tgccgcgaccc	ttcgacgccc	cagcagtgcc	tgagcagcca	agtccctgct	360
tgcacagagg	gcaaccaccca	ccagacccac	aagatcaagg	agctggccgc	cttcgctccc	420
cgcagaggag	gcaggataga	cgaaggaggt	gaggtgtacc	ggcatcacct	ggagcagatg	480
tacaagctgt	gcggcccggt	ccaagcgctg	gtgagtagct	acatcaagca	ccagaacccc	540
cagctgctgt	gcctgttctg	cagccacagc	ttcaagccgc	ggagggccga	ccagacccac	600
gcacagaact	tctcctccgc	cgtgaagtag	cgggtccagg	tcctccttgt	ccgtgccccc	660
gccttccctg	cctgcgcctc	cctactgaac	acggcgtgtg	atggggccag	cggaacattc	720
gcctcaggca	ccactgtccc	cctggccctg	ccactgtgtg	gcactgggtc	agccacaccc	780
gacaatggca	ccacccctgg	ggcggagggc	tggggcagc	tgttggggct	actcccccag	840
acatggcgg	agaagctgtg	tgaggccctg	gcctttgggc	agagccacca	gacggggctc	900
gtgggaactg	gcctactcac	ctgcctgtgt	gcaatgctgc	tggctggccg	cacccaggtc	960
cgaggagatg	atgcctctct	caactgcctg	tggccctccc	tgttggggct	gacctgggtc	1020
gagcagcacc	tgagggccgc	ctgccttagc	tggtagaca	cgtcccaagt	cagcaccaca	1080
tcttctgtgt	gcctgggttg	cttcacggcg	gtgtggccca	caagggaaggc	aacggggccc	1140
cggaggttcc	ggcccccagg	gtcagagagg	cagccc			1176

<210> 72
 <211> 1491
 <212> DNA
 <213> Homo sapiens

<400> 72

atggggcgtg	ggcggcgctc	cgcgtacggc	ggcttccctg	cggctggcgt	gggtgggtc	60
ttcctgctgg	agccagagct	gccaggctcc	ggcttccctg	ctctctggag	ctcgtctgtg	120
ctggggcccg	cgcccgccgc	cccgggaccc	gtctcccccg	agggcccggt	ggcggcagcc	180
tgggaagggc	tcctcgtggc	gccagtcagg	cgttggcgcc	gggtggcagt	gggagtcac	240
gcctgtgttg	atgtgggtgt	ctcagggttg	aagctcttgc	agccacttgg	ccctagtcct	300
gggaatggga	aagatcacag	cattctgcac	tcaagggaatg	atctgggaag	agccttcatt	360
cacttcacgt	gggaaggagg	agctgtctag	cgtctctcca	gtgataagga	aactttccac	420
gacatggccc	aggttgccgc	agagtcccca	ggagccacag	actatgtagg	aggaaatgca	480
gctttaattg	gacagaaatt	tgcagccaac	tcagatttaa	aggtctctct	ttggcgctca	540
gttggcccaa	ggctaacatg	gcttcttgat	gacatgtctc	tgttccccc	agagtcttg	600
cagggaagtg	atgagttcca	cctcatttta	gagtatcaag	caggggagga	gtggggccag	660
ttaaaagctc	cccatgccaa	cggattccat	ttctctccag	acctctccaa	cgggggccatg	720
aatatgtctg	aggtgtctgt	gtctagcttg	gaggagtttc	agccagacct	ggtgtctctc	780
tctggattgc	acatgatgga	gggacaaagg	aaggagctcc	agagggaagag	actcttggag	840
gttgtaacct	ccatttctga	cattcccaac	ggtattccag	ttcacctaga	gctggccagt	900
atgactaaca	ggagctccat	gagcagcatt	gtccatcagg	aggtctttcc	cgcgttgact	960
tcctttgggc	tgaatgaaca	ggagctgtta	ttctccaccc	agtcagccct	tggacctcac	1020
tcttctctct	cttctctgga	cggctgtctc	gagtgaggga	tggtcagtag	cactctcttc	1080
tggatcttga	aagaaacatg	gagagtagaa	agcagagcct	cggatctcac	caggatccat	1140
ttccacacgc	cgtcttacca	cattctggca	actgttgatg	gacactgggc	caaccagctg	1200
gcagccgtgg	ctgcaggagg	tgcgtgtgtg	gggacacagg	cctgcgcacc	agaaaccata	1260
gacaccagcc	gagtgctctc	gagggcacc	caagagttca	tgaacttcca	ttcggaggca	1320
ggctccagga	ttgtattaaa	cccaaaacag	ccagttagtag	aatggcacag	agagggaata	1380
tccttcacct	ccacaccagt	attgggtgtg	aaagacccca	ttcgaactgt	agcccttggg	1440
gatgcacatt	cagccgaagg	actctcttat	tccgaagta	caccttcacta	t	1491

<210> 73
 <211> 1251
 <212> DNA
 <213> Homo sapiens

<400> 73
 atgctgggagc atttatttccg ggtcgggattt cgggggtggcc cattcccagg caggetgcta 60
 ccgcccctcc gcttccagac atttccagct gtccaggtaact ctgatggcta ccgagctcc 120
 tccctccctcc gggccgtggc ccacctggcg tcccagctct gggcccacct cctcgagcc 180
 cccctagctc ccagatggag cccctctgcc tggctgtggg ttgggggagg cctgctaggg 240
 cccatggtao tgagtaagca tcccacacct tgccttgttg cctgtgtgga ggcagaagag 300
 gcccctccctg ccagctccac accccatgtc gtgggggtctc gctttaactg gaaactcttc 360
 tggcagtttc tgcaccccba cctgctgggc ctgggggtag ccgtctgtgt ggcttgggt 420
 gggccactcg tgaatgtaca gatcccccct cctctgggac agctggtaga ggtcgtggcc 480
 aagtaacaaa gggacccagt agggagtctt atgactgagt cccagaatct cagcaccac 540
 ctgcttctcc totatgggtt ccagggaact ctgaaccttg ggtacctgtt gctgtgttc 600
 caagttgggg agcgcatggc tgttgcacat cggaggggac tctccagctc cctgtccgg 660
 tactgcagac ccgaggggtc agagtgggga caagacatca cctctctga cgcacataag 720
 anagggcagc tggtagagcg ctgacaaact gaactgcagg agtttaagtc atccttcaag 780
 cttgtccatc ccagggggct gcgaagctgc accaggtgg caggtgtgct ggtgtccctg 840
 tccatgtgtc cgcacacgct ccagctgtgt ctgatggtgg ccacacagc cctgatggga 900
 gtgggcaccc tgatggggtc aggcctccga aaattgtctt gccagtgtca ggagcagatc 960
 gccagggcaa tggggttagc agacgaggcc ctgggcaatg tgcggactgt ggtgtgcttc 1020
 gccatggagc aacgggaaga gtagggctat ggggcagagg tggaaagctg ccgtgtccgg 1080
 gcagaggagc tgggtccggg cctgtgtctg ttccaaaggg tttccacat ccgttccac 1140
 tgcattggtc tgggtacccc atttattggg ggtccctctg tggccggaca gcagctgaca 1200
 gggggagacc tcatgtcttc cctgttggcc tcccagacaa tgcacaggct g 1260

<210> 74
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 74
 atgattccca accagcattaa tctcggagcc gggagccacc aaactgcagt tttcagaatg 60
 gcctggctgg acactgattt ggcacacatt cttccatctt ctgttcttcc cccattctgg 120
 gctaaagttag tagtgggata ggttgccatt gtgtgttttg caccgcagctc tgatggagac 180
 tttgtctctg atgactcaga agctattggt aacaataaagg ttgttgggtt tgtgggctgt 240
 gcagacatcc tgtgcgcctt gttcttcttg ttatcttccc ctggttaactg taaaggcttc 300
 agagaaaagta accaggaggg aggcattctt cccaccttct ggggtgtgtt gagtatcttc 360
 ctggggagcag tggccatgct gtgcacagag caagggatca ctgtgtctgg tttaaatgct 420
 gtatttgaca tcttggtgat aggcacattc aatgtcttgg aaattgtcca gaaggtacta 480
 cataaaggaca agtcattaga gaactctggc atgtccagg accggggctt cctcttcaga 540
 atgacccctg tccactctgg aggggtctgg atgtctaac tgcgtgtggg gatcatgggc 600
 accgggcctg cggccttccac ccaggttgga accccggctt cctctgttga cagcatgtct 660
 gtgagggcgg taaactacaa ttactactat ccattgaatg cctgggtgtt gctgtgtccc 720
 tgggtggctg tttctgattg gtcacatggc tgcattcccc ccatttaagtc catcagcgac 780
 tggagggtaa ttgcacttgc agcactctgg ctctgcctaa ctggcctgat atgcacagcc 840
 ctgtgtcttg aagacgggca caagagaagg atccttactc tgggcctggg acttctctgt 900
 atccatttcc tcccggcgag taacctgttc tccagagtgg gctcgtgtgt ccggagcgt 960
 gtctcttacc tcccagcat tgggtactgt gtgtgtgtga cttctggatt cggagccctg 1020
 agcaaacata ccaagaaaaa gaaactcatt gccgtgtctg tcttgggaat cttattcttc 1080
 aacacgtctg gatgtgtgtt gcgcagcggc gagtggcggg gtgaggaaca gcttttcaga 1140
 agtgcctctg ctgtgtgttc cctcaatgct aaggttcaat acaacatttg caaaaactg 1200
 gctgataaag ccaaccagac agctgcctac agatactacc gggaaagctgt aagatttaat 1260
 cccaaagtat tccatgcctt gaataatctt ggaaatatct taaaagaaaag gaatgagcta 1320
 caggaagctg aggagctgct gtcttttggt gttccaaatac agccagactt tgcctgtgct 1380
 tggatgaatc taggcatagt gcagaatagc ctgaaaagggt ttgaagcagc agagcaaggt 1440
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447

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<213> : Homo sapiens

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<222> : (193)...(1370)

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Val Leu Leu Tyr Arg Ile	Ala Arg Arg Met Lys	Pro Thr His Thr Met				
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Val Asn Cys Trp Phe Cys	Asn Gln Asp Thr Leu	Val Pro Tyr Gly Asn				
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<211> 2495

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 82

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Pro Glu Leu Pro Gly Ser Ala Leu Arg Ser Leu Trp Ser Ser Leu Cys
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Asp His Ser Ile Leu His Ser Arg Asn Asp Leu Glu Glu Ala Phe Ile
105 110 115 120
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His Phe Met Trp Lys Gly Ala Ala Ala Glu Arg Phe Phe Ser Asp Lys
125 130 135
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gag	ctg	goc	agt	atg	act	aac	agg	gag	ctc	atg	agg	agg	att	gtc	cat	965	
Glu	Leu	Ala	Ser	Met	Thr	Asn	Arg	Glu	Leu	Met	Ser	Ser	Ile	Val	His		
300							305					310					
gag	cag	gtc	ttt	ccc	goc	gtg	act	tcc	ttt	ggg	ctg	aat	gaa	cag	gag	1013	
Gln	Gln	Val	Phe	Pro	Ala	Val	Thr	Ser	Leu	Gly	Leu	Asn	Glu	Gln	Glu		
315						320						325					
atg	tta	ttt	ctc	acc	cag	tca	goc	tct	gga	act	cac	tct	tct	ctc	tct	1061	
Leu	Leu	Phe	Leu	Thr	Gln	Ser	Ala	Ser	Gly	Pro	His	Ser	Ser	Leu	Ser		
330						335					340						
tcc	tgg	aac	ggt	gtt	act	gat	gtg	ggc	atg	gtc	agt	gac	atc	ctc	ttc	1109	
Ser	Trp	Asn	Gly	Val	Pro	Asp	Val	Gly	Met	Val	Ser	Asp	Ile	Leu	Phe		
345					350				355				360				
tgg	atc	ttg	aaa	gaa	cat	ggg	agg	agt	aaa	agg	aga	goc	tgc	gat	ctc	1157	
Trp	Ile	Leu	Lys	Glu	His	Gly	Arg	Ser	Lys	Ser	Arg	Ala	Ser	Asp	Leu		
365						370						375					
acc	agg	atc	cat	ttc	cac	acg	ctg	gtc	tac	cac	atc	ctg	gca	act	gtg	1205	
Thr	Arg	Ile	His	Phe	His	Thr	Leu	Val	Tyr	His	Ile	Leu	Ala	Thr	Val		
380							385					390					
gat	gga	cac	tgg	goc	aac	cag	ctg	gca	goc	gtg	gct	gca	gga	gct	ggt	1253	
Asp	Gly	His	Trp	Ala	Asn	Gln	Leu	Ala	Ala	Val	Ala	Ala	Gly	Ala	Arg		
395						400					405						
gtg	gct	ggg	aca	cag	goc	tgc	goc	aca	gaa	acc	ata	gac	acc	agg	cga	1301	
Val	Ala	Gly	Thr	Gln	Ala	Cys	Ala	Thr	Glu	Thr	Ile	Asp	Thr	Ser	Arg		
410					415						420						
gtg	tct	ctg	agg	gca	ccc	caa	gag	ttc	atg	act	tcc	cat	tgc	gag	gca	1349	
Val	Ser	Leu	Arg	Ala	Pro	Gln	Glu	Phe	Met	Thr	Ser	His	Ser	Glu	Ala		
425					430				435					440			
ggc	tcc	agg	att	gta	tta	aac	cca	aac	aag	cca	gta	gta	gaa	tgg	cac	1397	
Gly	Ser	Arg	Ile	Val	Leu	Asn	Pro	Asn	Lys	Pro	Val	Val	Glu	Trp	His		
445							450						455				
aga	gag	gga	ata	tcc	ttc	cac	ttc	aca	cca	gta	ttg	gtg	tgt	aaa	gac	1445	
Arg	Glu	Gly	Ile	Ser	Phe	His	Phe	Thr	Pro	Val	Leu	Val	Cys	Lys	Asp		
460							465					470					
cat	att	cga	act	gta	ggc	ctt	gga	gat	goc	att	tca	gac	gaa	gga	ctc	1493	
Pro	Ile	Arg	Thr	Val	Gly	Leu	Gly	Asp	Ala	Ile	Ser	Ala	Glu	Gly	Leu		

475 480 485 1540

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Phe Tyr Ser Glu Val His Pro His Tyr

490 495

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<213> Homo sapiens

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gtcacc atg ctg gtg cat tta ttc cgg gtc ggg att cgg ggt ggc cca 104
Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro
1 5 10
ttc cca ggc agg ctg cta cgg ccc ctg cgg ttc cag aca ttc tca gct 150
Phe Pro Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala
15 20 25 30
gtc agg tac tct gat ggc tac cgc agc tcc tcc ctg ctg cgg gcc gtg 204
Val Arg Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val
35 40 45
gcc cac ctg cgg tcc cag ctg tgg gcc cac ctg cct cga gcc ccc cta 250
Ala His Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu
50 55 60
ggt cca aga tgg agc ccc tct gcc tgg tgg gtt ggg gga gcc ctg 300
Ala Pro Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu
65 70 75
cta ggt ccc atg gta ctg agt aag cat ccc cac ctg tgc ctt gtg gcc 348
Leu Gly Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala
80 85 90
ctg tgt gag gca gaa gag gcc cct cct gcc agc tcc aca ccc cat gtc 396
Leu Cys Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val
95 100 105 110
gtg ggt tct cgg ttt aac tgg aag ctg ttc tgg cag ttt ctg cac ccc 444
Val Gly Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro
115 120 125
cac ctg ctg gtc ctg ggg gta gcc gtc gtg ctg gcc ttg ggt gcc gca 492
His Leu Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala
130 135 140
cta gtg aac gta aag atc ccc ctg ctg ctg ggc cag ctg gta gag gtc 540
Leu Val Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val

145	150	155	
gtg gcc aag tac aca agg gac cac gta ggg agt ttc atg act gag tcc			588
Val Ala Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser			
160	165	170	
cag aat ctc agc acc cac ctg ctt atc ctc tat ggt gtc cag gga ctg			636
Gln Asn Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu			
175	180	185	190
ctg acc ttc ggg tac ctg gtg ctg ctg tcc cac gtt ggc gag cgc atg			684
Leu Thr Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met			
195	200	205	
ggt gtg gac atg cgg agg gcc ctc ttc ags tcc ctg ctc cgg tac tgc			732
Ala Val Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys			
210	215	220	
cag cag cag ggt gca gag ttg gga caa gac atc acc ttc ttt gac gcc			780
Gln Pro Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala			
225	230	235	
aat aag aca ggg cag ctg gtg ags cgc ttg aca act gac gtg cag gag			828
Asn Lys Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu			
240	245	250	
ttt aag tca tcc ttc aag ctt gtc atc tcc cag ggg ctg cga agc tgc			876
Phe Lys Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys			
255	260	265	270
acc cag gtg gca ggc tgc ctg gtg tcc ctg tcc atg ctg tcc aca cgc			924
Thr Gln Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg			
275	280	285	
ctc aag ctc ctg ctg atg gtg gcc aca cca gcc ctg atg gga gtg ggc			972
Leu Thr Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly			
290	295	300	
acc ctg atg ggc tca ggc ctc cga aaa ttg tct tgc cag tct cag gag			1020
Thr Leu Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu			
305	310	315	
cag atc gcc agg gca atg ggc gta gca gac gag gcc ctg ggc aat gtg			1068
Gln Ile Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val			
320	325	330	
egg act gtg cgt gcc ttc gcc atg gag caa cgg gaa gag gag cgc tat			1116
Arg Thr Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr			
335	340	345	350
ggg gca gag ctg gaa gcc tgc cgc tgc cgg gca gag gag ctg ggc cgc			1164
Gly Ala Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg			
355	360	365	
ggc atc gcc ttg ttc caa ggg ctt tcc aas atc gcc ttc aac tgc atg			1212
Gly Ile Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met			
370	375	380	
gtc ttc ggt acc cta ttt att ggg ggc tcc ctt gtg gcc gga cag cag			1260
Val Leu Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln			
385	390	395	
ctg aca ggg gga gac ctc atg tcc ttc ctg gtg gcc tcc cag aca gtg			1308
Leu Thr Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val			
400	405	410	
caa agg ctg tgacattcca tgcattggaag gacatccctt gacaggctgt gtg			1360
Gln Arg Leu			
415			
agctgccttt ccccatgctt gccacttcca gggatgacaa gctgacccct gtccccccac			1420
acccacccct tatagcttat tgccttgcgt tggctcaaaa ccaccgcctc agctgacct			1480
ctgggatgac cagagctgat caccagacag ctcaggggcg cctccccccc tccctctct			1540
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<211> 3269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (250)...(2209)

<400> 34

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agcaattgct gagagcatgc cgtatgcagc gctgtgaggc tcgagagaca agcagtgga      180
gagtgagggc ctgttttcac tctggattgt aaatctgagc ctactttctg cccctggaag      240
aggacagcat cagcatgga atg att cct aac cag cat aat gct gga gcc ggg      292
                Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly
                        1             5             10

agg cac caa cct gca gtt ttc aga atg gaa gtg ttg gac act gat ttg      340
Ser His Gln Pro Ala Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu
                        15             20             25

gat cac att ctt cca tct tct gtt ctt cct cca ttc tgg gct aag tta      388
Asp His Ile Leu Pro Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu
                        30             35             40

gta gtg gga tgg gtt gcc att gtg tgt ttt gca cgc agc tat gat gga      436
Val Val Gly Ser Val Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly
                        45             50             55

gac ttt gtc ttt gat gac tca gaa gct att gtt aac aat aag gtt gct      484
Asp Phe Val Phe Asp Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala
                        60             65             70             75

tgt gtt gtc ggc cgt gca gac ctg ctg tgt gcc ctg ttc ttc ttg tta      532
Gly Val Val Gly Arg Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Leu
                        80             85             90

tat ttc ctt ggc tac tgt aaa gca ttt aga gaa agt aac aag gag gga      580
Ser Phe Leu Gly Tyr Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly
                        95             100             105

ggg cat tct tcc acc ttc tgg gtg ctg ctg agt atc ttt ctg gga gca      628
Ala His Ser Ser Thr Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala
                        110             115             120

gtg gcc atg ctg tgc aaa gag gaa ggg atc act gtg ctg ggt tta aat      676
Val Ala Met Leu Cys Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn
                        125             130             135

ggg gta ttt gac atc ttg gtg ata ggc aaa ttc aat gtt ctg gaa att      724
Ala Val Phe Asp Ile Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile
                        140             145             150             155

gtc cag aag gta cta cat aag gac aag tca tta gag aat ctg gcc atg      772
Val Gln Lys Val Leu His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met
                        160             165             170

ctc agg aac ggg ggc ctg ctg ttc aga atg acc ctg ctg acc tct gga      820
Leu Arg Asn Gly Gly Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly
                        175             180             185

ggg gct ggg atg ctg tac gtg cgc tgg agg atc atg ggc aag ggc cgg      868
Gly Ala Gly Met Leu Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro
                        190             195             200

cag gcc ttc acc gag gtg gac aac cgg gcc tcc ttt gct gac agc atg      916
Pro Ala Phe Thr Glu Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met
                        205             210             215

ctg gtg agg gcc gta aac tac aat tac tac tat tca ttg aat gcc tgg      964
Leu Val Arg Ala Val Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp
                        220             225             230             235

ctg ctg ctg tgt gcc tgg tgg ctg tgt ttt gat tgg tca atg gcc tgc      1012
Leu Leu Leu Cys Pro Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys
                        240             245             250

atc ccc ctg att aag tcc atc agc gac tgg aag gta att gca ctt gca      1060
Ile Pro Leu Ile Lys Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala

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255	260	265	
gca ctc tgg ttc tgc cta att ggc ctg ata tgc caa gcc ctg tgc tct			1108
Ala Leu Trp Phe Cys Leu Ile Gly Leu Ile Cys Gln Ala Leu Cys Ser			
270	275	280	
gaa gac ggc cac aag aga agg atc ctt act ctg gcc ctg gga ttt ctc			1156
Glu Asp Gly His Lys Arg Arg Ile Leu Thr Leu Gly Leu Gly Phe Leu			
285	290	295	
gtt atc cca ttt ctc ccc ggc agt aac ctg ttc ttc cga gtg gcc ttc			1204
Val Ile Pro Phe Leu Pro Ala Ser Asn Leu Phe Phe Arg Val Gly Phe			
300	305	310	
gtg gtc gcc gag cgt gtc ctc tac ctc ccc aag att ggg tac tgt ctc			1252
Val Val Ala Glu Arg Val Leu Tyr Leu Pro Ser Ile Gly Tyr Cys Val			
320	325	330	
ctg ctg act ttt gga ttc gga gcc ctg aac aaa cat acc aag aaa aag			1300
Leu Leu Thr Phe Gly Phe Gly Ala Leu Ser Lys His Thr Lys Lys Lys			
335	340	345	
aaa ctc att gcc gct gtc gtg ctg gga atc tta ttc atc aac aag ctg			1348
Lys Leu Ile Ala Ala Val Val Leu Gly Ile Leu Phe Ile Asn Thr Leu			
350	355	360	
aga tgt gtg ctg cgc agc gcc gag tgg cgg aat gag gaa cag ctt ttc			1396
Arg Cys Val Leu Arg Ser Gly Glu Trp Arg Ser Glu Glu Gln Leu Phe			
365	370	375	
aga agt gct ctg tct gtg tgt ccc ctc aat gct aag gtt cac tac aac			1444
Arg Ser Ala Leu Ser Val Cys Pro Leu Asn Ala Lys Val His Tyr Asn			
380	385	390	
att gcc aaa aac ctg gct gat aaa gcc aac cag aca gct gac atc age			1492
Ile Gly Lys Asn Leu Ala Asp Lys Gly Asn Gln Thr Ala Ala Ile Arg			
400	405	410	
tac tac cgg gaa gct gta aga tta aat ccc aag tat gtt ctt gcc atg			1540
Tyr Tyr Arg Glu Ala Val Arg Leu Asn Pro Lys Tyr Val His Ala Met			
415	420	425	
aat aat ctt gga aat atc tta aaa gaa agg aat gag cta cag gaa gct			1588
Asn Asn Leu Gly Asn Ile Leu Lys Glu Arg Asn Glu Leu Gln Gln Ala			
430	435	440	
cag gag ctg ctg tct ttg gct gtt caa ata cag cca gac ttt gcc gct			1636
Glu Glu Leu Leu Ser Leu Ala Val Gln Ile Gln Pro Asp Phe Ala Ala			
445	450	455	
cag tgg atg aat cta gcc ata gtg cag aat aac ctg aaa cgg ttt gaa			1684
Ala Trp Met Asn Leu Gly Ile Val Gln Asn Ser Leu Lys Arg Phe Glu			
460	465	470	
gca gca gag caa agt tac cgg aca gca att aaa cac aga agg aaa tac			1732
Ala Ala Glu Gln Ser Tyr Arg Thr Ala Ile Lys His Arg Arg Lys Tyr			
480	485	490	
cca gac tgt tac tac aac ctc ggg cgt ctg tat gca gat ctc aat cgc			1780
Pro Asp Cys Tyr Tyr Asn Leu Gly Arg Leu Tyr Ala Asp Leu Asn Arg			
495	500	505	
cac gtg gat gcc ttg aat ggc tgg aga aat gcc acc gtg ctg aaa cca			1828
His Val Asp Ala Leu Asn Ala Trp Arg Asn Ala Thr Val Leu Lys Pro			
510	515	520	
gag cac agc ctg gcc tgg aac aac atg att ata ctc ctc gac aat aca			1876
Glu His Ser Leu Ala Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr			
525	530	535	
ggt aat tta gcc caa gct gaa gca gtt gga aga gag gca ctg gaa tta			1924
Gly Asn Leu Ala Gln Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu			
540	545	550	
ata cct aat gat cac tct ctc atg ttc tgc ttg gca aac gtc ctg ggg			1972
Ile Pro Asn Asp His Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly			
560	565	570	
aaa tcc cag aaa tac aag gaa tct gaa gct tta ttc ctc aag caa att			2020
Lys Ser Gln Lys Tyr Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile			
575	580	585	

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tat cat cgt tgg gga cat cta gac ttg gcc aag aaa cac tat gaa atc 2116
tyr his arg trp gly his leu asp leu ala lys lys his tyr glu ile
605 610 615
tcc ttg cag cta gac ccc acg gca tca gga act aag gag aat tac ggt 2164
ser leu gln leu asp pro thr ala ser gly thr lys glu asn tyr gly
620 625 630 635
ctg ctg aga aga aag cta gaa cta atg caa aag aaa gct gtc tcat 2210
leu leu arg arg lys leu glu leu met gln lys lys ala val
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Met ile his leu gly his ile leu phe leu leu leu leu pro val
1 5 10 15
gct gca gct cag acg act cca gga gag aga tca tca ctc cct gcc ttt 158
ala ala ala gln thr thr pro gly glu arg ser ser leu pro ala phe
20 25 30
tac cct ggc act tca ggc tat cgt tcc gga tgt ggg tcc ctc tat ctg 166
tyr pro gly thr ser gly ser cys ser gly cys gly ser leu ser leu
35 40 45
ccg ctc ctg gca ggc ctc gtg gct gct gat gag gtg gca tcc ctg ctc 184
pro leu leu ala gly leu val ala ala asp ala val ala ser leu leu
50 55 60
acc gtg ggg ggg gtg ctc ctg tgc gca cgc cca ggc cgc agc ccc gcc 202
ile val gly ala val phe leu cys ala arg pro arg arg ser pro ala
65 70 75
caa gaa gat ggc aaa gtc tac atc aac atg cca ggc agg gcc tgaacc 250
glu glu asp gly lys val tyr ile asn met pro gly arg gly
80 85 90
tctgcagct tggacctttg actttctgac ctctcactct ggatggtg tctgtggaca 410

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458

<210> 86

<211> 1712

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (180)...(1487)

<400> 86

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tggcagcacc cagcccccgc cgtccgggtgc tgaaccacct gctgggtggt ctcttcggc	179
atg ggc tcc tgg gct gcg gtc aat ggg atc tgg gtg gag cta cct gtg	227
Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val	
1 5 10 15	
gtg gtc aaa gag ctt cca gag ggt tgg agc ctc ccc tct tac gtc tct	275
Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser	
20 25 30	
gtg ctt gtg gct ctg ggg aac ctg ggt ctg ctg gtg gtg acc ctc tgg	323
Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp	
35 40 45	
agg agg ctg gcc cca gga aag gac gag cag gtc ccc atc cgg gtg gtg	371
Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val	
50 55 60	
cag gtg ctg ggc atg gtg ggc aca gcc ctg ctg gcc tct atg tgg cag	419
Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His	
65 70 75 80	
cat ctg gcc cca gtg gca gga cag ttg cat tct gtg gcc ttc tta gca	467
His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala	
85 90 95	
ctg cca ttt gtg ctg gca ctg gca tgc tgt gcc tcc aat gtc act ttc	515
Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe	
100 105 110	
ctg ccc ttc ctg agc cag ctg cca cct cgc ttc tta cgg tca ttc ttc	563
Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe	
115 120 125	
ctg ggt caa ggc ctg agt gcc ctg ctg ccc tgc gtg ctg gcc cta gtg	611
Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val	
130 135 140	
cag ggt gtg ggc cgc ctg gag tgc ccg cca gcc ccc atc aac ggc acc	659
Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr	
145 150 155 160	
cct ggc ccc ccg ctg gac ttc ctt gag agt ttt ccc gcc agc acc ttc	707
Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe	
165 170 175	
ttc tgg gca ctg act gcc ctt ctg gtc gct tca gct gct gcc ttc cag	755
Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln	
180 185 190	
ggt ctt ctg ctg ctg ttg ccg cca cca cca tct gta ccc aca ggg gag	803
Gly Leu Leu Leu Leu Leu Pro Pro Pro Ser Val Pro Thr Gly Glu	
195 200 205	
tta gga tca ggc ctg cag gtg gga gcc cca gga gca gag gaa gag gtg	851
Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val	
210 215 220	
gaa gag tcc tca cca ctg caa gag cta cca agc cag gca gca ggc acc	899
Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr	
225 230 235 240	
acc ctt ggt cca gac cct aag gcc tat cag ctt cta tca gcc cgc agt	947

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Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser
      245      250      255
gac tgc ctg ctg ggc atg ttg gcc gcc aac aac gcg ctg acc aat ggc      995
Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly
      260      265      270
gtg ctg cct gcc gtg gag agc ttt tcc tgc tta ccc tac ggg cgt ctg      1043
Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu
      275      280      285
gcc tac cac ctg gct gtg gtg ctg ggc agt gct gcc aat ccc ctg gcc      1091
Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala
      290      295      300
tgc ttc ctg gcc atg ggt gtg ctg tgc agg tcc ttg gca ggg ctg ggc      1139
Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly
      305      310      315      320
gac ctg tct ctg ctg ggc gtg ttc tgt ggg ggc tac ctg atg gcc ctg      1187
Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu
      325      330      335
gaa gtc ctg agc ccc tgc ccc ccc ctg gtg ggc acc tgc gcc ggg gtg      1235
Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val
      340      345      350
gac ctg gtg gtg ctg tcc tgg gtg ctg tct ctt ggc gtg ttc tcc tac      1283
Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr
      355      360      365
gtg aag gtg gca gcc agc tcc ctg ctg cat gcc ggg ggc cgg ccg gcc      1331
Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala
      370      375      380
tgc ctg gca gcc ggc gtg gcc atc cag gtc gcc tct ctg ctg gcc gct      1379
Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala
      385      390      395      400
gac gct atg ttc ccc ccg acc agc atc tat cac gtg ttc cac agc aga      1427
Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg
      405      410      415
aag cac tgt gca gac ccc tgt gac tcc tgaggctggg cagggtggga cccccc      1480
Lys Asp Cys Ala Asp Pro Cys Asp Ser
      420      425
tccccaacac ctgtttttct ctcaatgtg ccaccatgcc tgagtgcctg cagccccaga      1540
ggcccgcaaa cgtgtacact cgtggacacc tacacaactc ataggagatc ctggtttccc      1600
aggtgggga agggcaagga gaagccttgg acacagggac cagtgggggc tgtagggaaa      1660
gacctgagc ctgggaaccta catgtggtt gcgtaataaa acatttgtat tt      1712

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<110> 37
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 <112> DNA
 <113> Homo sapiens

<120>
 <121> CDS
 <122> (53)...(502)

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Met
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gag act ttg tac cgt gtc ccc ttc tta gtg ctg gaa tgt ccc aac ctg      103
Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn Leu
5 10 15
aag ctg aag aag ccc ccc tgc ttg cac atg ccc ccg gcc atg act gtg      151
Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr Val
20 25 30
tat gct ctc gtg gtg gtg tct tac ttc ctc atc acc aga gga ata att      199
Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile Ile

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35          40          45
tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg ast gat gaa      247
Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp Glu
50          55          60          65
cat ggg cat cag agg cca gta ggt ttc ttg gcc tac aga gta aat gga      295
His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn Gly
70          75          80
caa tat att atg gaa gga ctt gpa tcc agc ttc cta ttt aca atg gga      343
Gln Tyr Ile Met Gln Gly Leu Ala Ser Ser Phe Leu Phe Thr Met Gly
85          90          95
ggg tta ggt ttc ata atc atg gac cga tgg aat gca cca aat atc cca      391
Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile Pro
100          105          110
aaa ctc aat aga ttc ctt ctt atg ttc att gga ttc gtc tgt gtc cta      439
Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val Leu
115          120          125
ctg agt ctt ttc atg got aga gta ttc atg aga atg aaa ctg ccg ggc      487
Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro Gly
130          135          140          145
tat ctg atg ggt tagagtgcct ttgagaagaa atcagtggat actggatttg c      540
Tyr Leu Met Gly

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tctgtcgaat gaagtttttaa aggtcgtacc aatcctctaa tatgaaatgt ggaaaagaat      600
gaagagcagc agtaaaagaa atattctagt aaaaaacagg aagcgtattg aagcctggac      660
tgaattttct tcttggtatt aaagagacaa gtttatcaca gaattttttt tctcgtcggc      720
ctattgctat accaatgatg ttgagtggca tttctttttt agtttttcat taaaatatat      780
tccatctctc caactataat atcaataaaa gtgattattt tttaacaacc tcttaacatt      840
ttttggagat gaattttctg attttcagaa attaacataa atccagaag caagatttcg      900
taagctgaga actctggaca gttgatcaga tttactatg ctgccttgcg ttttaactaga      960
gtgtgtgatg gtgattattt taagataagt atgtaaaaat gtttcttgaa caataagatg      1020
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 <211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (222)...(1412)

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gtgagaaaaa cattctaata gctttattct gacatacggg ggtatggaga gcttgaagga      120
gtcagagagg tgcccagcta agactgaat gccatcaccc tcccagggc tctgcagttt      180
tctcgtggg aaccttgat ggattgttg ttgcttgaga a atg gcg atg atc      243
Met Ala Met Ile
-
gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag agt      281
Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys Arg Lys Ser
5          10          15          20
cca ttg ctg ttg aaa ctc ata ggt gtt gtc ttt gct gtg ctt cta ttt      349
Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val Leu Leu Phe
25          30          35
tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt aat tgg cct      377
Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys Asn Trp Pro
40          45          50
gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca cgt gag cct      425
Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr Arg Glu Pro
55          60          65
gtg ctc aaa gat atg ttt ttg gct gac acc cat ttg ctt ggg gaa tta      483

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Val	Leu	Lys	Ala	Met	Phe	Leu	Ala	Asp	Thr	His	Leu	Leu	Gly	Glu	Phe	
70						75					80					
cta	ggc	caa	agg	ctg	gac	aaa	tta	cga	agg	gaa	agg	cag	atg	gag	aga	521
Leu	Gly	His	Trp	Leu	Asp	Lys	Leu	Arg	Arg	Glu	Trp	Gln	Met	Glu	Arg	
85						90				95					100	
ggg	ttc	cag	aca	gct	ctg	tgg	tta	ctg	cag	ccg	gaa	gtc	gtc	ttc	atc	569
Ala	Phe	Gln	Thr	Ala	Leu	Trp	Leu	Leu	Gln	Pro	Glu	Val	Val	Phe	Ile	
				105					110					115		
ctg	ggg	gat	atc	ttt	gat	gaa	ggg	aag	tgg	agg	acc	cct	gag	gcc	tgg	617
Leu	Gly	Asp	Ile	Phe	Asp	Glu	Gly	Lys	Trp	Ser	Thr	Pro	Gln	Ala	Trp	
			120					125					130			
ggg	gat	gat	gtg	gag	agg	ttt	cag	aaa	atg	ttc	aga	cac	cca	agt	cac	665
Ala	Asp	Asp	Val	Glu	Arg	Phe	Gln	Lys	Met	Phe	Arg	His	Pro	Ser	His	
			135				140					145				
gta	cag	ctg	aag	gta	gtt	gct	gga	aac	cac	gac	att	ggc	tta	cac	tat	713
Val	Gln	Leu	Lys	Val	Val	Ala	Gly	Asn	His	Asp	Ile	Gly	Phe	His	Tyr	
150						155					160					
gag	atg	aac	aca	tac	aaa	gta	gaa	ggc	ttt	gag	aaa	gtg	tta	agg	ttt	761
Glu	Met	Asn	Thr	Tyr	Val	Glu	Arg	Phe	Glu	Lys	Val	Phe	Ser	Ser		
165					170				175					180		
gaa	aga	ctg	ttt	ttt	tgg	aaa	ggg	att	aac	ttt	gtg	atg	gtc	aac	agg	809
Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val	Met	Val	Asn	Ser	
			185					190					195			
gtg	ggg	ctg	aac	ggg	gat	ggc	tgt	ggc	atc	tgc	ttt	gaa	aca	gaa	gca	857
Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser	Glu	Thr	Glu	Ala	
			200					205					210			
gag	ctc	att	gaa	gtt	ttt	caa	aga	ctg	aac	tgg	ttc	cga	gag	gaa	cgt	905
Glu	Leu	Ile	Gln	Val	Ser	His	Arg	Leu	Asn	Cys	Ser	Arg	Gln	Ala	Arg	
		215					220					225				
ggc	ttc	agg	agg	tgt	gaa	cct	ggg	cct	ctg	ctg	ccc	agg	ttt	ggc	cct	953
Gly	Ser	Ser	Arg	Cys	Gly	Pro	Gly	Pro	Leu	Leu	Pro	Thr	Ser	Ala	Pro	
		230				235					240					
gtc	ctc	ctg	cag	cac	tac	cct	ctg	tat	ggg	aga	agt	gat	gct	aac	tgt	1001
Val	Leu	Leu	Gln	His	Tyr	Pro	Leu	Tyr	Arg	Arg	Ser	Asp	Ala	Asn	Cys	
245					250				255					260		
ttt	ggg	gaa	gac	gct	gct	cct	gaa	gag	gaa	agg	gac	atc	cca	ttt	aag	1049
Ser	Gly	Glu	Asp	Ala	Ala	Pro	Ala	Glu	Glu	Arg	Asp	Ile	Pro	Phe	Lys	
			265					270					275			
gag	aac	tat	gac	gtg	ctt	tca	ggg	gag	gca	tca	caa	aag	ctg	ctg	tgg	1097
Glu	Asn	Tyr	Asp	Val	Leu	Ser	Arg	Glu	Ala	Ser	Gln	Lys	Leu	Leu	Trp	
		280					285					290				
ggg	ctc	cag	ccg	agg	ctg	gtt	ctc	agt	ggc	caa	acg	cac	agg	ggc	tgc	1145
Trp	Leu	Gln	Pro	Arg	Leu	Val	Leu	Ser	Gly	His	Thr	His	Ser	Ala	Cys	
		295					300					305				
gag	gtg	cac	caa	ggg	ggc	cga	gtc	ccc	gag	ctc	agg	gtc	cca	ttt	tta	1193
Glu	Val	His	His	Gly	Gly	Arg	Val	Pro	Glu	Leu	Ser	Val	Pro	Ser	Phe	
		310				315					320					
agt	tgg	agg	aac	aga	aac	aac	ccc	agt	tta	atc	atg	ggg	agg	atc	acg	1241
Ser	Trp	Arg	Asn	Arg	Asn	Asn	Pro	Ser	Phe	Ile	Met	Gly	Ser	Ile	Thr	
		325			330				335					340		
ccc	aca	gac	tac	acc	ctc	tac	aag	tgc	tac	ctc	cca	cgt	gag	gat	gtg	1289
Pro	Thr	Asp	Tyr	Thr	Leu	Ser	Lys	Cys	Tyr	Leu	Pro	Arg	Glu	Asp	Val	
			345					350					355			
gtt	tta	atc	atc	tac	tgt	gga	gtg	gtg	ggc	tta	ctt	gtg	gtc	ctc	aca	1337
Val	Leu	Ile	Ile	Tyr	Cys	Gly	Val	Val	Gly	Phe	Leu	Val	Val	Leu	Thr	
		360					365					370				
ctc	act	cac	ttt	ggg	ctt	cta	ggc	tca	cct	ttt	ctt	ttt	ggt	ttg	aac	1385
Leu	Thr	His	Phe	Gly	Leu	Leu	Ala	Ser	Pro	Phe	Leu	Ser	Gly	Leu	Asn	
		375				380					385					
ctg	ctc	gga	aac	cgt	aag	aca	aga	tga	aga	gag	gag	gag	gag	gag	a	1431
Leu	Leu	Gly	Lys	Arg	Lys	Thr	Arg									

390 395
aatatcaaaag cccaaagaaat ggaacttttg gacagagatca tgttagaate aagtggatga 1490
tgagaccaat tacaggccgt ctctctgcac agcacagaaa ttctcaatca ctgaaatgag 1550
taactgcaaa ataaatagtt gattgtactg ttctcatgct ataaaaagtgg acaggtactc 1610
tacaac 1616

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (69)...(1121)

<400> 89
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tcagtgcc atg atc cgg cag gag cgc tcc aca tcc tac cag gag ctg 107
Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu
1 5 10
agt gag gag ttg gtc cag gtg gtt gag aac tca gag ctg gca gac gag 155
Ser Glu Glu Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu
15 20 25
cag cag aag gag aag gtc aga gtc caa ggt ccg ggt atc tta cca ggc 203
Gln Asp Lys Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly
30 35 40 45
ctg gag aag gag tcc gcc tcc agc aac atc cgc ttc agc aag gcc tgc 251
Leu Asp Ser Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys
50 55 60
ctg aag aac gtc ttc ccg gtc cta ctc atc ttc atc tac ctg ctg ctc 299
Leu Lys Asn Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu
65 70 75
atg gct gtg gcc gtc ttc ctg gtc tac cgg acc atc aca gac ttt cgt 347
Met Ala Val Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg
80 85 90
gag aaa ctc aag cac cct gtc atg tct gtg tct tac aag gaa gtg gat 395
Glu Lys Leu Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp
95 100 105
cgc tat gat gcc cca ggt att gcc ttg tac ccc ggt cag gcc cag ttg 443
Arg Tyr Asp Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu
110 115 120 125
ctc aac tgt aag cac cat tac gag gtc att cct cct ctg aca agc cct 491
Leu Ser Cys Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro
130 135 140
ggc cag ccg ggt gac atg aat tgc acc acc cag agg atc aac tac acc 539
Gly Gln Pro Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr
145 150 155
gac ccc ttc ttc aat cag act gtg aaa tct gcc ctg att gtc cag ggc 587
Asp Pro Phe Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly
160 165 170
ccc ccg gaa gtg aaa aag ccg gag ctg gtc ttc ctc cag ttc cgc ctg 635
Pro Arg Glu Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu
175 180 185
aac aag agt agt gag gac ttc agc gcc att gat tac ctc ctc ttc tct 683
Asn Lys Ser Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser
190 195 200 205
tct ttc cag gag ttc ctg caa agc cca aac agg gta gcc ttc atg cag 731
Ser Phe Gln Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln
210 215 220
acc tgt gag agt gcc tat ttc agc tgg aag ttc tct ggt gcc ttc cgc 779
Ala Cys Glu Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg

225 230 235
 acc tgg gtc aag atg tca ctg gta aag acc aag gag gag gat ggg cgg 827
 Thr Trp Val Lys Met Ser Leu Val Lys Thr Lys Glu Glu Asp Gly Arg
 240 245 250
 gaa gca gtg gag ttc cgg cag gag aca agt gtg gtt aac tac att gac 875
 Glu Ala Val Glu Phe Arg Gln Glu Thr Ser Val Val Asn Tyr Ile Asp
 255 260 265
 cag agg cca gct gcc aaa aaa agt gct caa ttg ttt ttt gtg gtc ttt 923
 Gln Arg Pro Ala Ala Lys Lys Ser Ala Gln Leu Phe Phe Val Val Phe
 270 275 280 285
 gaa tgg aaa gat cct ttc atc cag aaa gtc caa gat ata gtc act gcc 971
 Glu Trp Lys Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala
 290 295 300
 aat cct tgg aac aca att gct ctt ctc tgt ggc gcc ttc ttg gca tta 1019
 Asn Pro Trp Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu
 305 310 315
 ttt aaa gca gca gag ttt gct aaa ctg agt ata aaa tgg atg atc aaa 1067
 Phe Lys Ala Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys
 320 325 330
 att aga aag aga tac ctt aaa aga aga ggt cag gca acc agc cac ata 1115
 Ile Arg Lys Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile
 335 340 345
 agc tgaagtcacc tggcgttgtt tagagaactg tccacatcaa tgggagctgt ca 1170
 Ser
 350
 tcaactccac ttgttaaacg gagctatcaa caatcctgta ctcaactgaa gaaatggggc 1230
 ctgtctggga ggaacagcat gtaaaaactg aacttctaac cccgtcccaa aagaggcggg 1290
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 ctct cctgt ttgttccatt gtattgtatt aggttaagct ctactagggt aatgaaggct 1470
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 aaatctcaaa ctgagcttta aggcactag aaactagtaa ttaagtctct taatggactg 1710
 agtaaccacc taattgtcgg gotagaatgt ttgttgatgt atgagtttag attaacactc 1770
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 taacagggtaa ataaaaatta ataaaaaagg 1860

<210> 90
 <211> 783
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (245)...(706)

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 gggaaagtgg gactggcctt ggtacctggc tccagagctg caccacagagg cgtacagccc 180
 ggtgctggaa cggggcgggg ttggcgcaac taagggccac ggtacctgac cggccctgcc 240
 cagg atg act atc cac atc ctc atc ctg ctg ttg ctc ctc gcc ttc 286
 Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Ala Phe
 1 5 10
 tcc gcc caa ggg gac ctg gac act gca gcc agg cga ggc cag cac cag 334
 Ser Ala Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln
 15 20 25 30
 gtc ctt cag cac cgc ggg cac gtc tgc tac ctg ggc gta tgc cgg aac 388
 Val Pro Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr
 35 40 45

cac cgc ctg gag gag atc ata tac tgg att cgc tgt ctc cac caa gga 430
 His Arg Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly
 50 55 60
 gcc ctc ggg gaa ggc cag cca cga gcc cca gga ccc cta cag cta tgg 478
 Ala Leu Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp
 65 70 75
 ggc cgg cgg ctg gag cga ggc gga agc cgg gct cgg ttc cca gga ttc 526
 Ala Pro Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe
 80 85 90
 cgg cct gca ggc agg ggg cta ggc cag tgc cca gct cgg tgg gtg acc 574
 Arg Pro Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr
 95 100 105 110
 tgg ggc acg gct cgt ccc ctc ctc ggc ttc agt tgg cct atc tgt atg 622
 Ser Gly Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met
 115 120 125
 ctg gag att cta ctc cac att cct cct ccc cta act cca gcc cct gaa 670
 Leu Glu Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu
 130 135 140
 acc gtc ttc ccc agt ccc tcc cgg ggc tgc gac taggttgga ctagaag 720
 Thr Val Phe Pro Ser Pro Ser Pro Gly Cys Asp
 145 150
 cacacgggag caggctgggc gaagaacact gacgcacaga gccgaataaa caagagttcc 780
 gtg 783

<210> 91

<211> 403

<212> PRT

<213> Homo sapiens

<400> 91

Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr
 1 5 10 15
 Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
 20 25 30
 Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
 35 40 45
 Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
 50 55 60
 Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
 65 70 75 80
 Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
 85 90 95
 Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
 100 105 110
 Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val
 115 120 125
 Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
 130 135 140
 Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala
 145 150 155 160
 Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
 165 170 175
 Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
 180 185 190
 Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
 195 200 205
 Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
 210 215 220
 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
 225 230 235 240
 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly

	245		250		255
Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val					
260		265		270	
Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His					
275		280		285	
Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser					
290		295		300	

GI101-92
GI111-183
GI121-PET
GI121-Homo sapiens

Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser					
1		1		15	
Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala					
20		25		30	
Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn					
35		40		45	
Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Gln Leu					
50		55		60	
Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr					
65		70		75	
Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu					
80		85		90	
Phe Phe Pro Tyr Leu His Gln Asp Thr Gln Val Gln Tyr Gln Gln Asp					
95		100		105	
Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile					
110		115		120	
Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu					
125		130		135	
Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser					
140		145		150	
Ser Ala Leu Ala Trp Leu Thr Leu Gln Val Leu Ala Ile Leu Leu Ser					
155		160		165	
Ser Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val					
170		175		180	
Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met					
185		190		195	
Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Thr Cys					
200		205		210	
Lys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile					
215		220		225	
Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn					
230		235		240	
Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met					
245		250		255	
Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg					
260		265		270	

GI110-93
GI111-413
GI121-PET
GI121-Homo sapiens

Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly Leu					
1		5		10	
Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys Pro Tyr Thr Lys					
20		25		30	

Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp Leu Leu Tyr His
 35 40 45
 Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Pro Pro Gly Val Val
 50 55 60
 Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro
 65 70 75 80
 Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys Phe Tyr Ser Gln
 85 90 95
 Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp
 100 105 110
 Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr
 115 120 125
 Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys
 130 135 140
 Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala
 145 150 155 160
 Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser
 165 170 175
 Ala Phe Ala Ile Ile Val Phe Arg Val Glu Leu Cys Leu Phe Leu Gly
 180 185 190
 Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val Ser Val Val Arg
 195 200 205
 Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr
 210 215 220
 Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr Trp Pro Glu Gly
 225 230 235 240
 Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp Gly
 245 250 255
 Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg Gly Leu
 260 265 270
 Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr
 275 280 285
 His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu
 290 295 300
 Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu
 305 310 315 320
 Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys
 325 330 335
 Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu
 340 345 350
 Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe
 355 360 365
 Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His Gln Leu Val Pro
 370 375 380
 Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala Ala Ala Gln Thr
 385 390 395 400
 Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp Arg Tyr Asp Lys
 405 410 415
 Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala Tyr Thr His Ile
 420 425 430
 Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr Arg Asp Thr His
 435 440 445
 Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val Ser Leu Asn Leu
 450 455 460
 Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr Lys Leu Val Leu
 465 470 475 480
 Leu Glu Arg Leu Pro Arg Pro Ser
 485

<210> 94

<211> 152

<212> PRT

<213> Homo sapiens

<400> 94

```

Met Trp Pro Pro Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly
 1           5           10           15
Gly Ser Arg Pro Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro
      20           25           30
Ala Arg Ala Phe Leu Cys Ser Leu Lys Gly Arg Leu Leu Ala Glu
      35           40           45
Ser Gly Leu Ser Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala
      50           55           60
Ser Ala Phe Leu Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr
      65           70           75           80
Phe Leu Phe Ala Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu
      85           90           95
Cys Trp Pro Met Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile
      100           105           110
Tyr Phe Ala Ile Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala
      115           120           125
Ser Lys Ala Ala Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala
      130           135           140
Thr Asp Phe Tyr Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln
      145           150           155           160
Gly Asp Ser Ala Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn
      165           170           175
Ser Asp Ser Asp Ser Asp
      180

```

<210> 95

<211> 184

<212> PRT

<213> Homo sapiens

<400> 95

```

Met Asp Gly Leu Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn
 1           5           10           15
Leu Val Thr Glu Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu
      20           25           30
Lys Arg Tyr Leu Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu
      35           40           45
Leu Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val
      50           55           60
Tyr Pro Ala Tyr Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp
      65           70           75           80
Asp Asp Thr Val Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly
      85           90           95
Leu Ala Glu Phe Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr
      100           105           110
Tyr Val Gly Lys Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro
      115           120           125
Trp Asn Gly Ala Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe
      130           135           140
Leu Arg His His Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly
      145           150           155           160
Arg Ala Leu Asp Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser
      165           170           175
Gln Thr Pro Gln Pro Lys Asp Lys
      180

```

<210> 96

<211> 140
 <212> PFT
 <213> Homo sapiens

<400> 96

```

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu Val Met Val Ser
 1          5          10          15
Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg Asp His Thr Phe
 20          25          30
Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu Val Asn Gly Leu
 35          40          45
Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser Ser Val Ile Arg
 50          55          60
Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu Tyr His Ile Thr
 65          70          75          80
Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu Ser Glu Leu Phe
 85          90          95
Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu Ala Pro Leu Met
100          105          110
Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly Leu Arg Tyr Leu
115          120          125
Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn
130          135          140
    
```

<410> 97
 <411> 152
 <412> PFT
 <413> Homo sapiens

<400> 97

```

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
 1          5          10          15
Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 20          25          30
Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 35          40          45
Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 50          55          60
His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65          70          75          80
Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr
 85          90          95
Ser Ser Arg Lys Pro Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu
100          105          110
Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr
115          120          125
Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly
130          135          140
Val Arg Ile Phe Gly Ile Asn Lys Tyr
145          150
    
```

<410> 98
 <411> 173
 <412> PFT
 <413> Homo sapiens

<400> 98

```

Met Ala Ala Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val
 1          5          10          15
Gly Val Leu Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu
 20          25          30
    
```

Ile Ser Thr Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu
 35 40 45
 Pro Met Arg Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr
 50 55 60
 Ile Arg Ile Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys
 65 70 75 80
 Phe Met Leu Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Asn Ser
 85 90 95
 Pro Glu Ser Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro
 100 105 110
 Ser Val Ala Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val
 115 120 125
 Ser Gly Ser Leu Thr Pro Gln Pro Thr Gln Pro Pro Pro Lys Pro Lys
 130 135 140
 Thr Met Gly Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln
 145 150 155 160
 Lys Phe Glu Lys Lys Ser Val His Asn Lys Ala Tyr Phe
 165 170

0100: 99
 0110: 75
 0120: PRT
 0130: Homo sapiens

0400: 99
 Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met Asn Ala Gly
 1 5 10 15
 Ala Val Leu Asn Phe Lys Leu Lys Lys Asp Thr Gln Gly Phe Gly
 20 25 30
 Leu Glu Ser Arg Glu Pro Ser Thr Gly Asp Asn Ile Arg Glu Phe Leu
 35 40 45
 Leu Ser Leu Arg Tyr Phe Arg Ile Phe Ile Ala Leu Trp Asn Ile Phe
 50 55 60
 Met Met Phe Cys Met Ile Val Leu Phe Gly Ser
 65 70 75

0110: 100
 0111: 189
 0121: PRT
 0131: Homo sapiens

0400: 100
 Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly His Trp
 1 5 10 15
 Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr Ala Trp
 20 25 30
 Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala Gln Arg
 35 40 45
 Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu Ala Thr
 50 55 60
 Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg Val Ser
 65 70 75 80
 Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu Ser Leu
 85 90 95
 Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr Arg Glu
 100 105 110
 Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser Ser Gln
 115 120 125
 Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro Ala Asp
 130 135 140
 Pro Phe Ala Val Pro Glu Gly Arg Ser Gln Asp Ala Arg Gly Tyr

145

150

155

<210> 101
 <211> 909
 <212> DNA
 <213> Homo sapiens

<400> 101
 atggaggcag agcagcgggc ggcgggcgggg gccagcgaag gggcgacccc tggactggag 60
 gggtgccc ccgttgctcc ccgcctggc acgcgggccc caggccgat ccccaaatct 120
 ggccctgagc cttaagaggag gcaccttggg acgctgctcc agcctacggc caacaagttc 130
 ccccttcggg cgttcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca 240
 gggggggccc ggcacatcca cccctacagc gacttcgggt tttaactggga cctgacatg 300
 ctgctgctga tggctggggaa cctcatcgtc ctgctgtgg gcacacccc cttcaaggag 360
 gagaactccc cgccctggat cgtcttcaac gtatgtgtg atactttctt cctactggat 420
 gggtgctca atttcggaac gggcatcgct gtggaggagg gtgctgagat cctgctggca 480
 cggcgggcca ccgcacgcgc ctacctggc acctggttcc tggttgacct catctcttct 540
 atcctgttgg attacatctt cctagtggct gagctggagc caccggttga cgtcagggtc 600
 caaaaaagg ccaggggccc accgctcggt cgtttacca agatcctaa cctgctgagg 660
 ctgctcgccc cctcccgccc catccgctac atacaacagt gggaggagat ctttcacatg 720
 acctatgaac tggccagtgc tgtggttcgc atcttcaacc tcatggggat gatgctgctg 780
 ctatgctact gggatggctg tctgcagttc ctgggtgccca tgcgcaggga cttccctccc 840
 gctgctggg cctccatcaa ccacatggtg gtgagaagtc ccacagctc tgcctttctt 900
 ggcccttct 909

<210> 102
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 102
 atggcggacc cccaccagct cctcgatgac acaagttcag ccagagacag gggctatggg 60
 ggccaggggg caccctgggtg cctgagttat cctgcagccc ctccacagcc ccctgcagcc 120
 ctccctggctg acccggtgtc caacatggcc atggcctatg ggagcagccc ggccgcgcag 180
 ggcaagggagc tggctggataa gaacatcgac cgtttcctcc ccatcaccaa gctcaagtat 240
 caatttgcct tggacacccc gtatgtgggc agaaagctgg gctgctgtt cttcccttac 300
 ctacaccagg actgggaagt gcagtaacca cagggaacccc cgggtggccc ccgctttgac 360
 ggcactgccc cggacotcta cctccagca atgcttttca tcaactacgt cttgggtggc 420
 ggtcttgggc tggggaccca ggatagggtc tcccagacc tcttggggct gcaagcgagc 480
 caagccctcg cctggctgac cctggagggt ctggccatcc tgcctagccc ctatctgttc 540
 actgtcaaca ccgacctcac caccatcgac ctgggtggcc tcttgggcta caaatatgtc 600
 ggcatgattg cgggggtccc catgggccc ctcttgggga agattggcta ctacctggtg 660
 ctgggctggt gctgcgtaga catctttgtg ttcattgacc ggacgctgcg gctgaagatc 720
 ctggcagacg cagcagctga gggggctccc gtgctgagg ccgggaacca gctgcgcctg 780
 caactgacca tggcggttgc ggcgggcag cctatgctca tgaactggct cactttccac 840
 tggctgccc 849

<210> 103
 <211> 1464
 <212> DNA
 <213> Homo sapiens

<400> 103
 atggctggaa aggggtccatc aggcaggcgg cccctgctgc tggggctgct ggtggccgta 60
 ggcactgtcc acctggtcat ctgtccctac aaaaaagtgg aggagagctt caacctgcag 120
 ggcacacatg acctgctcta ccactggcaa gacctggagc agtaacacca tcttgagttc 180
 ccgggagctg tcccaggga gttcctcggg ccagtggtga tgcagtggt ctcagacccc 240
 gggttttacg tgccttccgt gttagaaatg tccaaagttt actctcagct aatagttaga 300
 ggagtgcctt gactcgggt gatttttqga ctctggacgt tacaaaaagg agtgagacgg 360
 caacttcggg ccattgctgg caccatgttc tgcctgggta cggccatcca gtccacatg 420
 atgttctact gcaagggaa atgtgcacat gtgctcgcac tgcctgtagt cctgctggac 480

ctcggggcct	ggctggggca	cgagtggggc	cgtttcatct	ggtgtgcagc	cttcggccatc	540
atcgtggtca	gggtggagct	gtgcctgttc	ctggggcctcc	tgtgtgtgct	ggccttgggc	600
aacggaaagg	tttctgtagt	cagagccctt	cggcaaggccg	tcggggcagg	gatcctctgt	660
ttaggaactga	cgggttgctgt	ggactcttat	ttttgggggc	agctcacttg	gcgggaaggga	720
aagggtgcttt	ggtacaacac	tgtcttgaaac	aaaagctcca	actgggggac	ctccccgctg	780
ctgttgtaact	tctactcagc	cctgcccgcg	ggcctgggct	gcagcctgct	cttcctccccc	840
ctgggtcttgg	tagacagaaag	gaagcagcgg	cggacgggtgc	tgggaactggg	cttcctatggc	900
ctctactccc	tcctggccaca	caaggagcta	cgtttcatca	tctatgcctt	ccccatgctc	960
aacatcacgg	ctggccagagg	ctgctctctac	ctgctgaata	actataaaaa	gtcttggtgtg	1020
tacaaagcag	ggtctctgct	tgtgatcgga	cacctctgtg	tgaatggccg	ctactcagcc	1080
acgttcctgt	atgtgtccca	tttcaactac	ccaggtggcg	tggcaatgca	gaggctggac	1140
cagtggtgtc	ccccccagac	agacgtccct	ctgcacattg	acgtggcagc	cggcccagaca	1200
gggtgtgtct	ggtttctcca	agtcaacagc	gcctggagggt	acgacaagag	ggaggatgtg	1260
cagtggggga	caggcatgct	ggcatacaca	cacatctcca	tggaggcggc	ccctgggctc	1320
ctgttcctct	acaggggac	acacgggggc	ctggccaggcg	tgggggggac	cacaggtgtg	1380
agtggaaccc	tgacccaaact	gccccctccc	aacgtccacc	tgcagacaaa	gttggtgctt	1440
ctgttagagge	tcccccgggc	gtcc				1464

<21> - 104

<21> - 546

<21> - DNA

<21> - Homo sapiens

<40> - 114

atgttgccac	ccagacccga	cccgaccccg	gaacccaggc	ctggccgggg	ctcccgctcc	60
agcctggggg	cccccggggg	ccggcccccg	ctggccgggg	gggttttccc	ctgcctctcc	120
aaaacccgac	tcctgtctgg	cgagtcgggt	ctctcattca	tcacttttat	ctgctatgtg	180
gggtctccag	catctgcctt	cctcacagcg	cctctgtctg	agttcctgct	ggccttgtae	240
tccctcttgg	ctgatgccat	gcagctgaat	gacaaagtgg	agggtttgtg	ctggcccatg	300
atgtacttcc	cgccctgggt	cccgccgggc	ctcactctat	ttgttatctc	catcacgggc	360
atcctcaagt	actcggatgg	ggcttcacaa	gcgcctgggg	tgtttggctt	ctttgtctac	420
atcctgttgg	caactgattt	ctacctgata	tttaacggag	tggccaaatt	cctcaaaaac	480
gggtactctg	cagatgagac	cacagccccc	aaagacagag	aaagagaattc	cgactcggac	540
tcttcc						546

<21> - 116

<21> - 552

<21> - DNA

<21> - Homo sapiens

<40> - 116

atgtacgggc	tgaggcagcg	cgtggagcac	ttcctggagg	aaaggaaact	ggtcacccgaa	60
gtgtgggggg	cgctggaggc	caagacccgg	gtggagaagg	ggatatctgc	tgcaggagcc	120
gtcactctgc	taagcctgta	tctgtctgtc	ggctacggag	cgtctctgct	gtgcaatctc	180
atcctatttg	tgtaccccgc	atatgcctca	atcaaaagcta	tcagagagcc	aagcaaggac	240
gacacacatg	cttggtctcc	ctactgggtg	gtgtacggcc	tgtttgggct	ggccgagttc	300
tccctggatc	cactcctgtc	ctggttccct	ttctaactac	tgggcaagtg	cgccttccctg	360
tgtgtctgca	tggtctccag	gccttggaac	ggggctctca	tgtgttatca	gcgcgtcctg	420
ggttgctgtg	tcctaaggca	ccacgggggc	gtagacagaa	tcctgaacga	cctcagcggg	480
cgaactcttg	acgcggcggc	cgggaataaac	aggaaactca	agccaagcca	gaccccgag	540
cggagggaca	ag					552

<21> - 116

<21> - 420

<21> - DNA

<21> - Homo sapiens

<40> - 116

atgagccggt	tcctgaatgt	gttaagaaat	tggctgggtta	tgggtgtccat	catagccatg	60
gggaacacgc	tgcagagctt	cagagacac	acttttctct	atgaaaagt	ctacactggg	120
aagccaaaac	ttgtgaatgg	ctcccaagct	cggacatttg	ggatctgac	gttgctctca	180

tcagtgtatc	gctgcctctg	tgcattgac	attcacaaca	agacgtctc	tcacatcaca	240
ctctggacct	tctctcttgc	cctggggcat	tctctctctg	agttgtttgt	ctatggaaact	300
gcagctccca	cgattggcgt	cctggcacc	ctgatgggtg	caagttctct	cctcctgggt	360
atgttggtcg	ggctccggt	tctagaagta	gaaccagtat	ccagacagaa	gaagagaaac	420

<210> 107

<211> 459

<212> DNA

<213> Homo sapiens

<401> 107

atgaacgttg	gagttgccc	cagtgaagtg	aatccaaata	ccgtgtctat	gaacagccgg	60
ggtatgtgg	tgacatatgc	attgggagtt	ggcttgcctc	atattgtctt	actcagcatt	120
ccctctctca	gtgttctctg	tgtttggact	ttaacaaata	ttatacatat	tctgggggatg	180
taagtatttt	tgcattgcagt	gaaagggaaca	cctttcgaaa	ctcctgacca	gggtaaagca	240
agggtcccaa	ctcattggga	acaaactggac	tatggagtac	agtttacatc	tccacggaaq	300
cttttcacaa	ctctctcaat	aattctatat	tctctggcaa	gtttctatac	gaagtatgat	360
ccaactcaat	ctcctctaaa	cacagcttct	ctcctgagtg	tactaatctc	caaaatgcca	420
caactcaatg	gtgttctggat	ctttggaatt	aataagtat			459

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<211> 519

<212> DNA

<213> Homo sapiens

<401> 108

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<212> DNA

<213> Homo sapiens

<401> 109

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<212> DNA

<213> Homo sapiens

<401> 110

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 1 5 10 15
 cct gga ctg gag ggg gtg cct ccc gtt get ccc cgg cct ggg acc ggg 216
 Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
 20 25 30
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 Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
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 Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
 50 55 60
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 Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
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 Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
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 Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
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 Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
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 Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
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 245 250 255

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 1112 DNA
 1113 Homo sapiens

1121
 1121 CDS
 1122 (56)...(907)

<400> 112

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1      5      10      15
cgg gcc tat ggg gcc cag cgg gca cct ggt ggc ctg agt tat cct gca      151
Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala
20      25      30
gcc tct ccc aag ccc cat gca gcc ttc ctg gct gac ccc gtg tcc aac      199
Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn
35      40      45
atg gcc atg gcc tat ggg agc agc ctg gcc ggc cag gcc aag gag ctg      247
Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Gln Leu
50      55      60
gtg gat aag aac atc gac cgc ttc atc ccc atc acc aag ctg aag tat      295
Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr
65      70      75      80
aac ttt gct ggg gac acc atg tat ctg gcc aga aag ctg gcc ctg ctg      343
Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu
85      90      95
ttc ttc ccc tac cta cag cag gac tgg gaa gtg cag tac caa cag gac      391
Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp
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Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile
115      120      125
cca gca atg ggt ttc atc acc tac att ctg ctg gct ggt att gcc ctg      487
Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu
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Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser
145      150      155      160
tca gcc ctg gcc tgg ctg acc ctg gag ggg ctg gcc atc ctg ctg agc      583
Ser Ala Leu Ala Trp Leu Thr Leu Gln Val Leu Ala Ile Leu Leu Ser
165      170      175
ctc tat ctg gtc act gtc aac acc gac ctg acc acc atc gac ctg gtg      631
Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val
180      185      190
gcc ttc tgg gcc tac aaa tat ctg ggg atg att gcc ggg gtc ctg atg      679
Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met
195      200      205
ggc ctg ctg ttc ggg aag att gcc tac tac ctg gtg ctg gcc tgg tgc      727
Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys
210      215      220
tgc gta gcc atc ttt gtg ttc atg atc cgg acc ctg cgg ctg aag atc      775
Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile
225      230      235      240
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Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn
245      250      255
cag ctg cgc atg tac ctg acc atg ggc gtg ggc ggc ggc cag cct atg      871
Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met
260      265      270
ctc atg tac tgg ctg acc ttc cag ctg gtg cgg tgagcgcgcc cgtcga      920
Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg
275      280
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cagccccgcc cccaacccaa ggtgatgaga gatctccagc tgcaacagcc abgcgccag      1100
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<211> E339

<212> DNA

<213> Homo sapiens

<220>

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<222> 253)... (1719)

<400> 113

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tggagt'gga gtgctaaccg ctggtgtctc gcactgttgg cctgtgaagg tacgtgaagc      240
tgaag'ctg ga atg gct gga aag ggg tca tca ggc agg cgg ccc ctg      288
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ctg ctg ggg ctg ctg gtg gcc gta gcc act gtc cac ctg gtc atc tgt      336
Leu Leu Gly Leu Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys
          15          20          25
ccc ta' acc aaa gtg gag gag agt ttc aac ctg cag gcc aca cat gac      384
Pro Tyr Thr Lys Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp
          30          35          40
ctg ctg tac cac tgg caa gac ctg gag cag tac gac cat ctt gag ttc      432
Leu Leu Tyr His Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe
          45          50          55          60
ccc aga gtc gtc ccc agg agt ttc ctg cgg cca gtg gtg atc gca gtc      480
Pro Gly Val Val Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val
          65          70          75
ttc tct agc ccc cgg att tac gtg ctt tgg ctg tra gaa atg tcc aag      528
Phe Ser Ser Pro Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys
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tct ta' tct cag cta ata gtt aga gga ctg ctt gga ctg gcc gtc att      576
Phe Tyr Ser Gln Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile
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ttt gga ctg tgg acg tta caa aag gaa gtg aga cgg cac ttc ggg gcc      624
Phe Gly Leu Trp Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala
          110          115          120
atg gtr gcc acc atg ttc tgc tgg gtg acg gcc atg cag ttc cac ctg      672
Met Val Ala Thr Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu
          125          130          135          140
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Met Phe Tyr Cys Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val
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gtc ctg ctg gcc ctg gcg gcc tgg ctg cgg cac gag tgg gcc cga ttc      768
Val Leu Leu Ala Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe
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atc tgr ctg tca gcc ttc gcc atc atc gtg ttc agg gtg gag ctg tgc      816
Ile Trp Leu Ser Ala Phe Ala Ile Ile Val Phe Arg Val Glu Leu Cys
          175          180          185
ctg ttc ctg ggc ctg ctg ctg ctg ctg gcc ttg gcc aac cga aag gtt      864
Leu Phe Leu Gly Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val
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tct gta gtc aga gcc ctt cgs cac gcc gtc ccg gca ggg atc ctg tgt      912
Ser Val Val Arg Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys
          205          210          215          220
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Leu Gly Leu Thr Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr
          225          230          235
tgg cca gaa gga aag gtg ctt tgg tac aac act gtc ctg aac aaa agc      1008
Trp Pro Glu Gly Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser
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Asp Arg Arg Thr His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala	
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Val Ser His Phe Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His	
365 370 375 380	
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Gln Leu Val Pro Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala	
385 390 395	
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415 420 425	
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Tyr Thr His Ile Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr	
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<222> (102)...(650)

<400> 114

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                                     Met Trp Pro Pro
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gac ccc gac ccc gac ccg gac ccc gag cct gcc ggc ggc tcc cgt ccc      161
Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly Gly Ser Arg Pro
   5               10               15               20
ggc ccc ggc gtc ccc ggg ctc cgc gcc ctg ctg ccg gcc cgg gct ttc      209
Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro Ala Arg Ala Phe
               25               30               35
ctc tgc tct ctc aaa ggc cgc ctc ctg ctg gcc gag tgc ggt ctc tca      257
Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu Ser Gly Leu Ser
   40               45               50
ttc atc act ttt atc tgc tat gag gcg tcc tca gca tct gcc ttc ctc      303
Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala Ser Ala Phe Leu
   55               60               65
aca gcc cct ctg ctg gag ttc ctg ctg gcc ttg tac ttc ctc ttt gct      353
Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr Phe Leu Phe Ala
   70               75               80
gat gcc atg car ctg aat gac aag tgg cag gcc ttg tgc tgg ccc atg      401
Asp Ala Met Glu Leu Asn Asp Lys Trp Glu Gly Leu Cys Trp Pro Met
   85               90               95
atg gac ttc ctg cgc tgt gtc acc gcc gcc ctc atc tac ttt gct atc      444
Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile Tyr Phe Ala Ile
   100              105              110
tcc atc acg gcc atc gcc aag tac tgc gat ggg gct tcc aaa gcc gct      497
Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala Ser Lys Ala Ala
   120              125              130
ggg ctg ttt gcc ttc ttc gat acc atc gtg ttt gca act gat ttc tac      541
Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala Thr Asp Phe Tyr
   135              140              145
ctg atc ttt aac gac gtg gcc aaa ttc ctc aaa caa ggc gac tct gca      593
Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Glu Gly Asp Ser Ala
   150              155              160
gat gag acc aca gcc cac aag aca gaa gaa gag aat tcc gac tgc gac      641
Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn Ser Asp Ser Asp
   165              170              175              180
tct gac tgaaggctg ggggtgtgct tggcaacctg agccacacag gcc      690
Ser Asp

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tccacccctg cgcctccag ggttcgctgg cgttggagcg gaggcctgga cttctgagtt      757
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ctaccaggct tgcctctcag ctacgacatg ttgaccacgc tgcgtatgag ggcctcttgg      870
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accatgacag ggttgcctcg ccaggccccg gtgggttttg ctgcacttgg tgcctctgcc     1110
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tgtgttcacc caacgattta taatgtgtat ctgtcttga tggaaatttg taacttttta     1590

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 1222> (149)...(703)

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 ggtgcccggga aaggggtggc cgtgcagggg ggtgggtggc ctgggtccgg ggcgagctcg 120
 ggcagccaaac cccggggggc tggggggc atg gac ggc ctg agg cag cgc gtg 172
 Met Asp Gly Leu Arg Gln Arg Val
 1 5
 gag cac ttc ctg gag caa agg aac ctg gtc acc gaa ctg ctg ggg ggc 220
 Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr Glu Val Leu Gly Ala
 10 15 20
 tgg gag gcc aag acc ggg gtg gag aag cgg tat ctg gct gca gga gcc 268
 Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr Leu Ala Ala Gly Ala
 25 30 35 40
 gtc act ctg cta agc ctg tat ctg ctg ttc ggc tac gga ggc tct ctg 316
 Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly Tyr Gly Ala Ser Leu
 45 50 55
 ctg tgc aat ctg atc gga ttt gtg tac ccc gca tat gcc tca atc aaa 364
 Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala Tyr Ala Ser Ile Lys
 60 65 70
 gct atc gag agc cca agc aag gac gac gac act gtg tgg ctg acc tac 412
 Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr Val Trp Leu Thr Tyr
 75 80 85
 tgg gtg gtg tac gcc ctg ttt ggg ctg gcc gac ttc ttc agc gat cta 460
 Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu Phe Phe Ser Asp Leu
 90 95 100
 ctg ctg tcc tgg ttc act ttc tac tac gtg ggc aag tgc gcc ttc ctg 508
 Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly Lys Cys Ala Phe Leu
 105 110 115 120
 ttg ttc tgc atg gct ccc agg ccc tgg aac ggg gct ctg atg ctg tat 556
 Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly Ala Leu Met Leu Tyr
 125 130 135
 gag cgc gtc gtg cgt ccg ctg ttc cta agg cac cac ggc gcc gta gac 604
 Gln Arg Val Val Arg Pro Leu Phe Leu Arg His His Gly Ala Val Asp
 140 145 150
 aga atc atg aac gac ctg agc ggg cga gcc ctg gac gcc gcc gcc gga 652
 Arg Ile Met Asn Asp Leu Ser Gly Arg Ala Leu Asp Ala Ala Ala Gly
 155 160 165
 ata acc agg aac gtc aag cca agc cag acc ccg cag ccg aag gac aag 700
 Ile Thr Arg Asn Val Lys Pro Ser Gln Thr Pro Gln Pro Lys Asp Lys
 170 175 180
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<213> Homo sapiens

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<222> (133)...(555)

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tggaggggag tc atg agc cgt ttc ctg aat gtg tta aga agt tgg ctg 168
Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu
1 5 10
gtc atg gtg tcc atc ata gcc atg ggg aac acg ctg cag agc ttc cga 216
Val Met Val Ser Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg
15 20 25
aac tac act ttt ctg tat gaa aag ctg tac act ggc aag cca aac ctt 264
Asp His Thr Phe Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu
30 35 40
gtg aat ggc ctg caa gct cgg acc ttt ggg atc tgg acg ctg ctg tca 312
Val Asn Gly Leu Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser
45 50 55 60
tca atg att cgc tgc ctg tgt gcc att gac att cac aac aag acg ctg 360
Ser Val Ile Arg Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu
65 70 75
tat cac atc aca ctg tgg acc ttc ctg ctg gcc ctg ggg cat ttc ctg 408
Tyr His Ile Thr Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu
80 85 90
tct cag tgg tat ttc gtc tat gga act gca gct ccc acg att ggc gtc ctg 456
Ser Glu Leu Phe Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu
95 100 105
gca ccc ctg atg gtg gca agt ttc tcc atc ctg ggt atg ctg gtc ggg 504
Ala Pro Leu Met Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly
110 115 120
ctc cgg tat cta gaa gta gaa cca gta tcc aga cag aag aag aga aac 552
Leu Arg Tyr Leu Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn
125 130 135 140
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g 1211

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<211> 1099
<212> DNA
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<220>

<221> CDS

<222> (183)...(644)

<400> 117

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tttatggata cattaagtca aatataagag tctgaactact tgacacactg gctcgagcaa      180
ac atg aac gtt gga gtt gcc cac agt gaa gtg aat cca aat acc cgt      225
Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg
1         5         10         15
gtc atg aac agc cgg ggt atg tgg ctg aca tat gca ttg gga gtt ggc      270
Val Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly
20        25        30
tgg ctt cat att gtc tta ctg agc att acc ttc ttc agt gtt cct gtt      325
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val
35        40        45
gct tgg act tta aca aat att ata cat aat ctg ggg atg tac gta ttt      370
Ala Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe
50        55        60
tgg cat gca gtg aaa gga aca cct ttc gaa act cct gac cag ggt aaa      415
Leu His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys
65        70        75
gca agc ctg cta act cat tgg gaa caa ctg gac tat gga gta cag ttt      460
Ala Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe
80        85        90        95
aca tct tca cga aag ttt ttc aca att tct cca ata att cta tat ttt      515
Thr Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe
100       105       110
atg gca agt ttc tat acg aag tat gat cca act cac ttc atc cta aac      565
Leu Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn
115       120       125
aca cct tct ctg ctg agt gta cta att ccc aaa atg cca caa cta cat      610
Thr Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His
130       135       140
ggc gtt cgg atc ttt gga att aat aag tat tgaaatgttt tgaaactga      660
Gly Val Arg Ile Phe Gly Ile Asn Lys Tyr
145       150
aaaaaaaaattt tacagctact gaattttotta taaggaagga gtgggttagta aactgcactg      720
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atttctqaag aggggcttta taagcaggct gggcaggccc agcttataag ttaaagggca      900
tcacagttag ggtgtagtag ataaattcaa ggaataaga gatttgtaag aaactaggac      960
cagcttaact tataatgaat gggcattgtg ttaagaaaag aacatttcca gtcattcagc      1020
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1090

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<211> 3489

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (227)...(748)

<400> 118

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ccattagggt taaggaagca cctacatact ctgtaactca gggaccaggt gggaacagct      180
gaagtgcagg agtggcttct tctttcagac cctctccagg agccac atg gct gcc      240

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Met Ala Ala

1

ttc ctg ata cag acc aag gac aac ccc atg aag gcc gtg ggt gtg ctg	232
Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val Gly Val Leu	
5 10 15	
gcc ggc acc atg gcc aac gtc gtg gcc atc act gtc ctc atc acc acc	231
Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu Ile Ser Thr	
20 25 30 35	
guc aac ttc tgg cgc aac aag aag tct aac aag gtc cgc cca atg cgg	230
Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu Pro Met Arg	
40 45 50	
cug gtu ctc cgc aag cgg acc agc ctt gcc ccc cgc acc acc ggc att	229
Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr Ile Arg Ile	
55 60 65	
gag tgc ctc aag tct aag agc acc aac gcc gct acc aag ttc atg ctc	228
Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys Phe Met Leu	
70 75 80	
aaa gta aaa ctt ccc act gag aac tct aac aac aac ggc cca aaa agc	227
Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Ser Pro Glu Ser	
85 90 95	
tct ctc ctc cgg aga gct cag gct ctc act cca cca acc agc atg ggc	226
Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro Ser Val Ala	
100 105 110 115	
cac agt act ggc gaa ggc cag tgg aac atg act act gtc tct agc act	225
Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val Ser Gly Ser	
120 125 130	
ctc act cag cag cgc aac cca acc cgc cca aac acc aac act atg gga	224
Leu Thr Pro Glu Pro Thr Gln Pro Pro Pro Lys Pro Lys Thr Met Gly	
135 140 145	
agc cgc gtc cag tca act cgc atc tct gag ctc aag cca aag ttt gag	223
Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln Lys Phe Glu	
150 155 160	
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Lys Lys Ser Val His Asn Lys Ala Tyr Phe	
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gcacagagag agaaaagtag aacagttctt tgcatttggc tctacttact aacaacctct	196

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 <211 - 931
 <212 DNA
 <213 Homo sapiens

<220
 <221 CDS
 <222 (25)...(252)

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Thr Leu Leu Met Asn Ala Gly Ala Val Leu Leu Phe Lys Leu Lys Lys
10 15 20 25
aag aac aag cag ggc ttt ggg gag gag tcc agg gag ccc agc aca ggt 147
Lys Asp Thr Gln Gly Phe Gly Glu Glu Ser Arg Glu Pro Ser Thr Gly
30 35 40
gac aac atc cgg gaa ttc ctg ctg agc ctg aga tac ttt cga atc ttc 185
Asp Asn Ile Arg Glu Phe Leu Leu Ser Leu Arg Tyr Phe Arg Ile Phe
45 50 55
atc aac ctg tgg aac atc ttc atg atg ttc tgc atg att gtg ctg ttc 243
Ile Ala Leu Trp Asn Ile Phe Met Met Phe Cys Met Ile Val Leu Phe
60 65 70
ggc tct tgaatccag cgatgaaac aggaactac tttcccggga tgcagagct c 300
Gly Ser
75
catt ctcca ttccgtatga cttcaagaat gtttttgacc agaaaaacga caaccttccc 360
agaaagtcca agctcgtggg ggggtgaaaa gtgttcgcca aggtgtgcat ggtttcccag 420
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cctgtataga cactaaattg ttagecaagz tgttgageta gttcctgggt aagtgtttcc 840
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 <212> DNA
 <213> Homo sapiens

<300>
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 <312> (66)...(547)

<400> 120
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 acgggg atg gaa ctg cct gct ggc aac ctg aag gtg att ctc cta ggt 100
 Met Gln Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly
 1 5 10
 aac tgg ctg ctg aca acc tgg ggc tgc att gta ttc tca ggc tcc tat 110
 His Trp Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr
 15 20 25 30
 pcc tgg ggc aac ttc acc atc ctg ggc ttc ggc gtg tgg gct gtg gct 200
 Ala Trp Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala
 35 40 45
 aac tgg gac tcc atc gac ggc ata aac atg ttc ctg ggt ggc ctg ctg 210
 His Arg Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu
 50 55 60
 gaa acc atc ttc ctg gac atc gta cac atc agc atc ttc taa cag cgg 301
 Ala Thr Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg
 65 70
 gaa ggc ctg aac gac acg ggc ggc ttc ggc gtg ggc atg ggc atc ctg 310
 Ala Ser Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu
 75 80 90
 aac tgg ctg ctg aag cag ctg ttc ttc ttc ttc gtc taa cac atg taa 320
 Ser Leu Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr
 95 100 105 110
 aag tag ggc ggc ggt gag ctg ctg gtc cac att ggt ttc ctg ggg taa 330
 Arg His Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser
 115 120 125
 aac tag gac cgt agt ggc taa caa aag att gac tca gaa gag gag ccc 340
 Ser Gln Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro
 130 135 140
 gaa tat ccc ttc gaa gtc caa gag ggc aag agt caa gat ggc cga ggc 341
 Ala Asp Pro Phe Ala Val Pro Gln Gly Arg Ser Gln Asp Ala Arg Gly
 145 150 155
 ttc tgaagcaga cagctgggc ccggccctgc ccggggcctt cctcgtgctt gggagg 360
 Tyr

tggtctagg gatgctcctg acctccgtct ctgggacta agatggaatg tgcaccagc 370
 tggggattg cctgaaccaa gaggcacgga gcccccatgg ccggccagat accatgcaca 380
 ctctgtccc gaactccctg aggcctccc tcccttcagg gcacccactg gtccccaggg 390
 tggacccagg gtctctcttt acctccatcc ccatggtggc accacagagg cctccagccg 400
 agtctgctt gattgttgcg agtcacgggc ttttaaggact gctgatgccc cctcaggcct 410
 ccccaagctt tgcctgggctt tgggtggaag ccggacagct tcaggtcctg ctacagccga 420
 gtagagctt ggcctgggag tgaggccccc cccctatcac tgcctgggta catggtgctt 1070
 aggtatgag ggcctggagg ccagaggtgt agcaaacctg tgaccaccca caacctacag 1080
 ctctctctt cagagcacag cattaagatt tgggghatto tgt 1120

<210> 121
 <211> 656
 <212> PRT
 <213> Homo sapiens

<400> 121
 Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu

1	5	10	15
Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp			
20	25	30	
Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln			
35	40	45	
Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe			
50	55	60	
Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp			
65	70	75	80
Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr			
85	90	95	
Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser			
100	105	110	
Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly			
115	120	125	
Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp			
130	135	140	
Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu			
145	150	155	160
Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp			
165	170	175	
His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro			
180	185	190	
Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp			
195	200	205	
Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile			
210	215	220	
Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly			
225	230	235	240
Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu			
245	250	255	
Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro			
260	265	270	
Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly			
275	280	285	
Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala			
290	295	300	
Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly			
305	310	315	320
Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys			
325	330	335	
Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly			
340	345	350	
Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile			
355	360	365	
Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro			
370	375	380	
Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu			
385	390	395	400
Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu			
405	410	415	
Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu			
420	425	430	
Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His			
435	440	445	
Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp			
450	455	460	
Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val			
465	470	475	480
Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn			
485	490	495	

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510
 Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525
 Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Ser Ser Leu Pro Glu Thr
 530 535 540
 Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555
 Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 560 565 570 575
 Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590
 Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605
 Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620
 Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<110> 121
 <111> 313
 <112> PRT
 <113> Homo sapiens

<410> 121
 Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
 1 10 15
 Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
 20 25 30
 Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
 50 55 60
 Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
 65 70 75 80
 Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
 85 90 95
 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
 100 105 110
 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
 115 120 125
 Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
 130 135 140
 His Ile Gly Val Asn His Leu Gly His Phe Leu Thr His Leu Leu
 145 150 155 160
 Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
 165 170 175
 Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
 180 185 190
 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
 195 200 205
 Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
 210 215 220
 Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
 225 230 235 240
 Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
 245 250 255
 Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
 260 265 270
 Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
 275 280 285

Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
 290 295 300
 Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
 305 310 315

<210> 123
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Ala Phe Thr Leu Tyr Ser Leu Leu Gln Ala Ala Leu Leu Cys Val
 1 5 10 15
 Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly
 20 25 30
 Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile
 35 40 45
 Lys Ser Gln Leu Met Asn Leu Ile Arg Ser Val Arg Thr Val Met Arg
 50 55 60
 Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu
 65 70 75 80
 Phe Gly

<210> 124
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 124
 Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu Leu
 1 5 10 15
 Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu Lys Val
 20 25 30
 Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu Val Gly
 35 40 45
 Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly Arg Glu
 50 55 60
 Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His Thr Gly
 65 70 75 80
 Lys Glu Leu Asp Lys Gly Val Gln Gly Leu Asn His Gly Met Asp Lys
 85 90 95
 Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys Glu Ala
 100 105 110
 Glu Lys Leu Gly His Gly Val Asn Asn Ala Ala Gly Gln Ala Gly Lys
 115 120 125
 Glu Ala Asp Lys Ala Val Gln Gly Phe His Thr Gly Val His Gln Ala
 130 135 140
 Gly Lys Glu Ala Glu Lys Leu Gly Gln Gly Val Asn His Ala Ala Asp
 145 150 155 160
 Gln Ala Gly Lys Glu Val Glu Lys Leu Gly Gln Gly Ala His His Ala
 165 170 175
 Ala Gly Gln Ala Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn
 180 185 190
 Gln Ala Ser Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser
 195 200 205
 Gly Ser Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser
 210 215 220
 Gly Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
 225 230 235 240
 Ser Val Ala Asn Ile Met Pro

245

<210> 125
 <211> 206
 <212> PRT
 <213> Homo sapiens

<400> 125

Met	Ala	Pro	Ser	His	Leu	Ser	Val	Arg	Glu	Met	Arg	Glu	Asp	Glu	Lys
1				5					10					15	
Pro	Leu	Val	Leu	Glu	Met	Leu	Lys	Ala	Gly	Val	Lys	Asp	Thr	Glu	Asn
		20						25					30		
Arg	Val	Ala	Leu	His	Ala	Leu	Thr	Arg	Pro	Pro	Ala	Leu	Leu	Leu	Leu
	35						40					45			
Ala	Ala	Ala	Ser	Ser	Gly	Leu	Arg	Phe	Val	Leu	Ala	Ser	Phe	Ala	Leu
	50					55					60				
Ala	Leu	Leu	Leu	Pro	Val	Phe	Leu	Ala	Val	Ala	Ala	Val	Lys	Leu	Gly
	65				70					75					80
Leu	Arg	Ala	Arg	Trp	Gly	Ser	Leu	Pro	Pro	Pro	Gly	Gly	Leu	Gly	Gly
			85					90						95	
Pro	Trp	Val	Ala	Val	Arg	Gly	Ser	Gly	Asp	Val	Cys	Gly	Val	Leu	Ala
		100						105					110		
Leu	Ala	Pro	Gly	Thr	Asn	Ala	Gly	Asp	Gly	Ala	Arg	Val	Thr	Arg	Leu
	115						120						125		
Ser	Val	Ser	Arg	Trp	His	Arg	Arg	Arg	Gly	Val	Gly	Arg	Arg	Leu	Leu
	130					135						140			
Ala	Phe	Ala	Glu	Ala	Arg	Ala	Arg	Ala	Trp	Ala	Gly	Gly	Met	Gly	Glu
	145				150					155					160
Pro	Arg	Ala	Arg	Leu	Val	Val	Pro	Val	Ala	Val	Ala	Ala	Trp	Gly	Val
			165					170						175	
Gly	Gly	Met	Leu	Glu	Gly	Cys	Gly	Tyr	Gln	Ala	Glu	Gly	Gly	Trp	Gly
		180						185					190		
Cys	Leu	Gly	Tyr	Thr	Leu	Val	Arg	Glu	Phe	Ser	Lys	Asp	Leu		
		195					200					205			

<210> 126
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 126

Met	Asp	Ala	Arg	Trp	Trp	Ala	Val	Val	Val	Leu	Ala	Ala	Phe	Pro	Ser
1				5					10					15	
Leu	Gly	Ala	Gly	Gly	Glu	Thr	Pro	Glu	Ala	Pro	Pro	Glu	Ser	Trp	Thr
		20						25					30		
Gln	Leu	Trp	Phe	Phe	Arg	Phe	Val	Val	Asn	Ala	Ala	Gly	Tyr	Ala	Ser
	35						40					45			
Phe	Met	Val	Pro	Gly	Tyr	Leu	Leu	Val	Gln	Tyr	Phe	Arg	Arg	Lys	Asn
	50					55					60				
Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	Leu	Val	Lys	Ala	Cys
	65				70					75					80
Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Ser	Asp	Glu	Val	Pro	Leu	Ala	Pro
			85						90					95	
Arg	Thr	Glu	Ala	Ala	Glu	Thr	Thr	Pro	Met	Trp	Gln	Ala	Leu	Lys	Leu
		100						105					110		
Leu	Phe	Cys	Ala	Thr	Gly	Leu	Gln	Val	Ser	Tyr	Leu	Thr	Trp	Gly	Val
	115						120						125		
Leu	Gln	Glu	Arg	Val	Met	Thr	Arg	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser
	130					135					140				
Pro	Gly	Glu	Arg	Phe	Thr	Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg
	145					150				155					160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 155 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255
 Ser Gly Pro Gln Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270
 Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
 275 280 285
 Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Pro
 290 295 300
 Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
 305 310 315 320
 Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
 325 330 335 340
 Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
 345 350 355
 Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
 360 365 370
 Ile Ile Met Phe Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
 375 380 385
 Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
 390 395 400
 Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
 405 410 415
 Gln Arg Gly Lys Lys Ala Val Pro Val Gln Ser Pro Val Gln Lys Val
 420 425 430

4110-127
 411-306
 412-PRT
 413-Homo sapiens

4400-127
 Met Gly His Asn Thr Leu Val Leu Pro Trp Val Leu Leu Thr Leu Cys
 1 5 10 15
 Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val Arg Met Glu Ala
 20 25 30
 Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe Leu Gly Ser Gly
 35 40 45
 Ser Ile Ser Leu Val Thr Val Ser Trp Gly Lys Pro Asp Gly Ala Gly
 50 55 60
 Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly Ile Arg Gln Trp
 65 70 75
 Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu
 80 85 90 95
 Ile Leu Gln Gly Ser Gly Ala Ser Ser Pro Cys Ala Asn Thr Thr Phe
 100 105 110
 Cys Lys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp Glu Ala Cys Gly
 115 120 125
 Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro
 130 135 140
 Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu Gly Val Ser Gly
 145 150 155 160

Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu Leu Arg Arg His
165 170 175
Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg Thr Ser Pro Gln
180 185 190
Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala Ser Gln Ala Ala
195 200 205
Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys Arg Pro Ala Thr
210 215 220
Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp Trp Ala Ser Leu
225 230 235 240
Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala Ala Trp Ala Ser
245 250 255
Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val Glu Asn Gly Leu
260 265 270
Tyr Ala Gln Ala Gly Gln Arg Pro Pro His Thr Gly Pro Gly Leu Thr
275 280 285
Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu Gly Pro Leu Gly
290 295 300
Val Arg
305

<210> 128
<211> 555
<212> PRT
<213> Homo sapiens

<400> 128
Met Gln Ser Cys Glu Ser Ser Gly Asp Ser Ala Asp Asp Pro Leu Ser
1 5 10 15
Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg Val Val Val Ile Gly Ala
20 25 30
Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala Leu Leu Glu Gln Gly Phe
35 40 45
Thr Asp Val Thr Val Leu Glu Ala Ser Ser His Ile Gly Gly Arg Val
50 55 60
Gln Ser Val Lys Leu Gly His Ala Thr Phe Glu Leu Gly Ala Thr Trp
65 70 75 80
Ile His Gly Ser His Gly Asn Pro Ile Tyr His Leu Ala Glu Ala Asn
85 90 95
Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu Arg Ser Val Gly Arg Ile
100 105 110
Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys Tyr Leu Thr Asn His Gly
115 120 125
Arg Arg Ile Pro Lys Asp Val Val Glu Glu Phe Ser Asp Leu Tyr Asn
130 135 140
Glu Val Tyr Asn Leu Thr Gln Gln Phe Phe Arg His Asp Lys Pro Val
145 150 155 160
Asn Ala Glu Ser Gln Asn Ser Val Gly Val Phe Thr Arg Glu Glu Val
165 170 175
Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp Pro Glu Ala Thr Lys Arg
180 185 190
Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu Lys Val Glu Ser Cys Glu
195 200 205
Ser Ser Ser His Ser Met Asp Glu Val Ser Leu Ser Ala Phe Gly Glu
210 215 220
Trp Thr Glu Ile Pro Gly Ala His His Ile Ile Pro Ser Gly Phe Met
225 230 235 240
Arg Val Val Glu Leu Leu Ala Glu Gly Ile Pro Ala His Val Ile Gln
245 250 255
Leu Gly Lys Pro Val Arg Cys Ile His Trp Asp Gln Ala Ser Ala Arg
260 265 270

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Pro Arg Gly Pro Glu Ile Glu Pro Arg Gly Glu Gly Asp His Asn His
275 281 285
Asp Thr Gly Glu Gly Gly Gln Gly Gly Glu Glu Pro Arg Gly Gly Arg
290 295 300
Trp Asp Glu Asp Glu Gln Trp Ser Val Val Val Glu Cys Glu Asp Cys
305 310 315 320
Glu Leu Ile Pro Ala Asp His Val Ile Val Thr Val Ser Leu Gly Val
325 330 335
Leu Lys Arg Gln Tyr Thr Ser Phe Phe Arg Pro Gly Leu Pro Thr Glu
340 345 350
Lys Val Ala Ala Ile His Arg Leu Gly Ile Gly Thr Thr Asp Lys Ile
355 360 365
Phe Leu Glu Phe Glu Glu Pro Phe Trp Gly Pro Glu Cys Asn Ser Leu
370 375 380
Gln Phe Val Trp Glu Asp Glu Ala Glu Ser His Thr Leu Thr Tyr Pro
385 390 395 400
Pro Glu Leu Trp Tyr Arg Lys Ile Cys Gly Phe Asp Val Leu Tyr Pro
405 410 415
Pro Glu Arg Tyr Gly His Val Leu Ser Gly Trp Ile Cys Gly Glu Glu
420 425 430
Ala Leu Val Met Glu Lys Cys Asp Asp Glu Ala Val Ala Glu Ile Cys
435 440 445
Thr Glu Met Leu Arg Gln Phe Thr Gly Asn Pro Asn Ile Pro Lys Pro
450 455 460
Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser Asn Pro Tyr Phe Arg Gly
465 470 475 480
Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser Gly Ala Asp Val Glu Lys
485 490 495
Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser Ser Lys Thr Ala Pro Met
500 505 510
Gln Val Leu Phe Ser Gly Glu Ala Thr His Arg Lys Tyr Tyr Ser Thr
515 520 525
Thr His Gly Ala Leu Leu Ser Gly Gln Arg Glu Ala Ala Arg Leu Ile
530 535 540
Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly Thr
545 550 555

```

> 129

> 250

> PRT

> Homo sapiens

> 129

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Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg
1 5 10 15
Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu
20 25 30
Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser
35 40 45
Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln
50 55 60
Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg
65 70 75 80
Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu
85 90 95
Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu
100 105 110
Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln
115 120 125
Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn
130 135 140

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Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln
155 150 155 160
Tyr Met Asn Thr Val Val Ser Thr Tyr Val Thr Thr Asn Val Ser Leu
165 170 175
Ile Pro Pro Arg Ser Glu Gln Leu Val Asn Phe Thr Gly Lys Ala Glu
180 185 190
Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu
195 200 205
Ile Leu Val His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile
210 215 220
Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr
225 230 235 240
Val Asp Cys Gly Gly Asn Ser Thr Ala Ile
245 250

<110> 130
<111> 174
<112> FRT
<113> Homo sapiens

<400> 130
Met Gln Ala Pro Ala Phe Arg Asp Lys Lys Gln Gly Val Ser Ala Lys
1 5 10 15
Asn Gln Gly Ala His Asp Pro Asp Tyr Gln Asn Ile Thr Leu Ala Phe
20 25 30
Lys Asn Gln Asp His Ala Lys Gly His Ser Arg Pro Thr Ser Gln
35 40 45
Val Pro Ala Gln Cys Arg Pro Ser Asp Ser Thr Gln Val Pro Cys
50 55 60
Trp Leu Tyr Arg Ala Ile Leu Ser Leu Tyr Ile Leu Leu Ala Leu Ala
65 70 75 80
Phe Val Leu Cys Ile Ile Leu Ser Ala Phe Ile Met Val Lys Asn Ala
85 90 95
Glu Met Ser Lys Glu Leu Leu Gly Phe Lys Arg Glu Leu Trp Asn Val
100 105 110
Ser Asn Ser Val Gln Ala Cys Glu Arg Gln Lys Arg Gly Trp Asp
115 120 125
Ser Val Gln Gln Ser Ile Thr Met Val Arg Ser Lys Ile Asp Arg Leu
130 135 140
Glu Thr Thr Leu Ala Gly Ile Lys Asn Ile Asp Thr Lys Val Gln Lys
145 150 155 160
Ile Leu Glu Val Leu Gln Lys Met Pro Gln Ser Ser Pro Gln
165 170

<110> 131
<111> 1908
<112> DNA
<113> Homo sapiens

<400> 131
atgaccacgt ggagcctcgg gaggagggcg gcccgcaagg tgggactcct gctgctggtc 60
gtcttggggt tcttggtgct tggcaggctg gactggagca ccttggtccc tctggggctc 120
ggccatcgac agctgggggt gcaggccaag ggctggaaat tcatgctgga ggattccacc 180
ttctggatct tggggggctc catccactat ttccgtgtgc ccaggggagta ctggaggggac 240
cgcttctgta agatgaaggc ctgtggcttg aacaccccca ccacctatgt tccgtgggaac 300
ctgcatgagc cagaaagagg caaatttgac ttctctggga acctggacct ggaggccttc 360
gtcttgatgg ccgcagagat cgggctgtgg gtgattctgc gtccaggccc ctacatctgc 420
agtggatgg acctcggggg ctgcccagc tggctactcc aagacctgg catgaggctg 480
aggacaactt acaagggtt caccgaagca gtggaccttt attttgacca ctgcatgtcc 540
agggtggtgc cactccagta caagcgtggg ggaacctatc ttgcctgtca ggtggagaat 600
gaatatggtt cctataataa agaccccgca tacatgacct acgtcaagaa ggcactggag 660

gaccgtggga	ttgtggaaat	gctccctgact	tcagacaaca	aggatggggt	gagcaagggg	720
attgtccagg	gagtcttggc	caccatcaac	ttgcagtraa	cacacgagct	gcagctactg	740
accaccttcc	tcttcaacgt	ccagjgggact	cagccccaga	tggatgatga	gtactggacg	840
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tgggttgagca	cgggaatcaa	ccaggtccatc	gtttctgagg	agaagatggc	gggccttgca	1860
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<210> 132
 <211> 984
 <212> DNA
 <213> Homo sapiens

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<210> 133
 <211> 246
 <212> DNA
 <213> Homo sapiens

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ggatttggag	aagagccggg	aattaaatca	cagctaatga	accttattctg	attctgtaaga	180
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tttgga						246

<210> 134
 <211> 741
 <212> DNA
 <213> Homo sapiens

<400> 131

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agcaatgag	agagagaggt	gggcaaggcc	ctggatggca	tcaacagtgg	aatcacgcct	180
gcccgaaggg	aagtggagaa	ggttttcaac	ggacttagca	acatggggag	ccacacccgg	240
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<210> 135

<211> 613

<212> DNA

<213> Homo sapiens

<400> 135

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gggggggggt	ccgttgaggt	gtgtggggct	ctgggtctgg	cccttggcac	aaatgcaggg	360
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tccggggccc	ggctcgttgt	cccggtggct	gtggccggct	gggggggtgg	agggatgctg	540
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<210> 136

<211> 1236

<212> DNA

<213> Homo sapiens

<400> 136

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gagagagcca	cccgatgtcg	gcaggccctg	aagctgctct	tctgtggcac	agggctccag	360
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1296

<210> 137

<211> 918

<212> DNA

<213> Homo sapiens

<400> 137

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<210> 138

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 138

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<210> 139

<211> 750
<212> DNA
<213> Homo sapiens

<400> 139
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gtggattctg gaggaaattc cacagctatt 750

<212> 140
<213> 122
<212> DNA
<213> Homo sapiens

<400> 140
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gagagacaga agagaggctg ggattccgtt cagcagagaa tcaaccatgt caggagcag 420
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acttggagg tgcgcagaa aatgccacag tctccacctc aa 522

<212> 141
<213> 1234
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (129)...(2039)

<400> 141
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aacacggg atg acc acg tgg agc ctc cgg cgg agg ccg gcc cgc acg ctg 170
Met Phe Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu
1 5 10
gga ctc ctg ctg ctg gtc gtc ttg gcc ttc ctg gtg ctt cgc agg ctg 218
Gly Leu Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu
15 20 25 30
gac tgg agc acc ctg gtc cct ctg cgg ttc cgc cat cga cag ctg ggg 266
Asp Trp Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly
35 40 45
ctg cag gcc aag gcc tgg aac ttc atg ctg gag gat tcc acc ttc tgg 314
Leu Gln Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp
50 55 60
acc ttc ggg gcc tcc atc cgc tat ttc cgt gtg ccc agg gag tac tgg 362
Ile Phe Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp

65	70	75	
agg gac cgc ctg ctg aag atg aag ggc tgt gcc ttg aac acc ctc acc			410
Arg Asp Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr			
20	85	90	
acc tat gtt cgc tgg aac ctg cat gag cca gaa aga gcc aaa ttt gac			453
Thr Tyr Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp			
95	100	105	110
ttc tct ggg aac ctg gac ctg gag gcc ttc gtc ctg atg gcc gca gag			505
Phe Ser Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu			
115	120	125	
atc ggg ctg tgg gtg att ctg cgt cca ggc ccc tac atc tgc agt gag			554
Ile Gly Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu			
135	135	140	
atg gac ctc ggg ggc ttg ccc agc tgg cta ctc caa gac cct ggc atg			602
Met Asp Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met			
145	150	155	
agg ctg agg acc act tac aag gcc ttc acc gaa gca gtg gac ctt tat			650
Arg Leu Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr			
160	165	170	
ttt gac cac ctg atg tcc agg gtg gtg cca ctc cag tac aag cgt ggg			693
Phe Asp His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly			
175	180	185	190
gga cct atc att gcc gtg cag gtg gag aat gaa tat ggt tcc tat aat			746
Gly Pro Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn			
195	200	205	
aaa gac ccc gca tac atg ccc tac gtc aag aag gca ctg gag gac cgt			794
Lys Asp Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg			
215	215	220	
ggc att gtg gaa ctg ctc ctg act tca gac aac aag gat ggg ctg agc			842
Gly Ile Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser			
225	230	235	
aag ggg att gtc cag gga gtc ttg gcc acc atc aac ttg cag tca acc			890
Lys Gly Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr			
240	245	250	
cac gag ctg cag cta ctg acc acc ttt ctc ttc aac gtc cag ggg act			933
His Glu Leu Gln Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr			
255	260	265	270
cag ccc aag atg gtg atg gag tac tgg acc ggg tgg ttc gac tgg tgg			986
Gln Pro Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp			
275	280	285	
gga gcc cct cac aat atc ttg gat tct tct gag gtt ttg aaa acc gtg			1034
Gly Gly Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val			
295	295	300	
tct gcc att gtg gac gcc gcc tcc tcc atc aac ctc tac atg ttc cac			1082
Ser Ala Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His			
305	310	315	
gga gcc acc aac ttt ggc ttc atg aat gga gcc atg cac ttc cat gac			1130
Gly Gly Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp			
320	325	330	
tac aag tca gat gtc acc agc tat gac tat gat gct gtg ctg aca gaa			1178
Tyr Lys Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu			
335	340	345	350
gcc ggc gat tac acc gcc aag tac atg aag ctt cga gac ttc ttc gcc			1226
Ala Gly Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly			
355	360	365	
tcc atc tca ggc atc cct ctc cct ccc cca cct gac ctt ctt ccc aag			1274
Ser Ile Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys			
370	375	380	
atg cag tat gag ccc ata aag cca gtc ttg tar ctg tct ctg tgg gac			1322
Met Pro Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp			
385	390	395	

gac ctc aag tac ctg ggg gag cca atc aag tct gaa aag ccc atc aac	1370
Ala Leu Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn	
400 405 410	
atg gag aac ctg cca gtc aat ggg gga aat gaa cag tcc ttc ggg tac	1418
Met Glu Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr	
415 420 425 430	
att ctc tat gag aac agc atc aac tgc tct ggc atc ctc agt ggt cac	1466
Ile Leu Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His	
435 440 445	
gtg cat gat cgg ggg cag gtg ttt gtg aac aca gta tcc ata gga ttc	1514
Val His Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe	
450 455 460	
ctg gac tac aag aca aca aag att gct gtc ccc ctg atc cag ggt tac	1562
Leu Asp Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr	
465 470 475	
acc gtg ctg agg atc ttc gtg gag aat ggt ggg cga gtc aac tat ggg	1610
Thr Val Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly	
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gag aat att gat gac cag cgc aaa ggc tta att gga aat ctc tat ctg	1658
Glu Asn Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu	
495 500 505 510	
aat gat tca ccc ctg aaa aac ttc aga atc tat agc ctg gat atg aag	1706
Asn Asp Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys	
515 520 525	
aag agc ttc ttt cag agc ttc ggc ctg gac aaa tgg agt tcc ctc cca	1754
Lys Ser Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Ser Ser Leu Pro	
530 535 540	
gaa aca ccc aca tta cct gct ttt tta tgg ggt agt tgg tcc atc agt	1802
Glu Thr Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser	
545 550 555	
tcn acc ctt tgt gac acc ttt ctg aag ctg gag ggc tgg gag aag ggg	1850
Ser Thr Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly	
560 565 570	
gtt gta ttc atc aat ggt cag aac ctt gga cgt tac tgg aac att gga	1898
Val Val Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly	
575 580 585 590	
ccc cag aag aag ctt tat ctc cca ggt ccc tgg tgg agc agc gga atc	1946
Pro Gln Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile	
595 600 605	
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Asn Gln Val Ile Val Phe Glu Gln Thr Met Ala Gly Pro Ala Leu Gln	
610 615 620	
ttc aag gaa acc ccc caa ctg ggc agg aac cag tac att aag tgag	2040
Phe Thr Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys	
625 630 635	
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tcttggcaga agccatgggc catgtctgca cctccaggga ggaggacaga agcccagct	3000

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<211> 2430

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<213> Homo sapiens

<220>

<221> CDS

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 cgggcacag atg gtt gag ctg atg ttc cgg ctg ttg ctg ctg ctt ctg ccc 111
 Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro
 1 5 10
 ttc ctt ctg tat atg gct gag ccc caa atc agg aaa atg ctg tcc agt 159
 Phe Leu Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser
 15 20 25 30
 ggg gta tgt aca tca aat gtt cag ctt cct ggg aaa gta gtt gtg gtc 207
 Gly Val Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val
 35 40 45
 aca gga gct aat aca ggt atc ggg aag gag aca gcc aaa gag ctg gct 255
 Thr Gly Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala
 50 55 60
 cag aga gga gct cga gta tat tta gct tgc cgg gat gtg gaa aag ggg 303
 Gln Arg Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly
 65 70 75
 gaa tta gtg gcc aaa gag atc cag acc acg aca ggg aac cag cag gtg 351
 Glu Leu Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val
 80 85 90
 ttg gta cgg aaa ctg gac ctg tct gat act aag tct att cga gct ttt 399
 Leu Val Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe
 95 100 105 110
 gct aag gcc ttc tta gct gag gaa aag cac ctg cac gtt ttg atc aac 447
 Ala Lys Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn
 115 120 125
 aat gca gga gtg atg atg tgt cgg tac tgg aag aca gca gat ggc ttt 495
 Asn Ala Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe
 130 135 140
 gag atc cac ata gga gtc aac cac ttg ggt cac ttc ctg cta acc cat 543
 Glu Met His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His
 145 150 155
 ctg cta cta gag aaa cta aag gaa tca gcc cca tca agg ata gta aat 591
 Leu Leu Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn
 160 165 170
 gtg tct tcc ctg gca cat cac ctg gga agg atc cac ttc cat aac ctg 639
 Val Ser Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu
 175 180 185 190
 cag ggt gag aaa ttc cac aat gca ggc ctg gcc tac tgt cac agc aag 687
 Gln Gly Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys
 195 200 205
 cta gcc aac atc ctg ttc acc cag gaa ctg gcc cgg aga cta aaa ggc 735
 Leu Ala Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly
 210 215 220
 tct gcc gtt acg acg tat tct gta cac cct ggc aca gtc caa tct gaa 783
 Ser Gly Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu
 225 230 235

ctg att cgg cac tca tct ctc atg aga tgg atg tgg tgg ctt ttc tcc 831
 Leu Val Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser
 240 245 250
 ttt ttc atc aag act cct cag cag gga gcc cag acc agc ctg cac tgt 879
 Phe Phe Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys
 255 260 265 270
 gac tca aca gaa ggt ctt gag att cta agt ggg aat cat ttc agt gac 927
 Ala Leu Thr Gln Gly Leu Gln Ile Leu Ser Gly Asn His Phe Ser Asp
 275 280 285
 tgt cat gtg gca tgg gtc tct gcc caa ggt cgt aat gag act ata gca 975
 Cys His Val Ala Trp Val Ser Ala Gln Ala Arg Asn Gln Thr Ile Ala
 290 295 300
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 Arg Arg Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
 305 310 315
 taccagg cagtgccagt tggacccaaq agaagaactgc agcagactac acagtaactac 1070
 tcttcaaaat gattctcttt caaggtcttc aaaaacttta gcacaaagag agcaaaact 1120
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 ctgacctgac atggtaact atggtaact taataatatt ttggggcatt tcttcaatt 1920
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 gttctgtct tgaactataa gctatattgt cagaatggt cacttttaagg aaaaataga 2170
 tttatctga taatagtgca gaataaatga attaatggtt taacttaattt atattgaact 2220
 gttatgaca aataaaatt cttcttctat 2270

010 - 143
 011 - 146
 012 - DNA
 013 - Homo sapiens

010 -
 011 - CDS
 012 - (34)...(131)

0400 - 143
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 ctctgggggg gctcgggag gac atg gcc ttt acc ctg tac tca ctg ctg 110
 Met Ala Phe Thr Leu Tyr Ser Leu Leu
 : :
 cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag gag 118
 Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Gln Gln
 11 15 20 25
 cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt gga 206
 Arg Phe Leu Lys Asn Ile Gly Trp Gly Trp Asp Gln Gly Ile Gly Gly
 30 35 40

[illegible]

Gly Ile Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val	
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aac aac gct gct gga cag gcc ggg aag gaa gca gac aaa gcg gtc caa	436
Asn Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln	
120 125 130 135	
ggg ttc cac act ggg gtc cac cag gct ggg aag gaa gca gag aaa ctt	484
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys Leu	
140 145 150	
ggc caa ggg gtc aac cat gct gct gac cag gct gga aag gaa gtg gag	532
Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu Val Glu	
155 160 165	
aag ctt ggc caa ggt gcc cac cat gct gct ggc cag gcc ggg aag gag	580
Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala Gly Lys Glu	
170 175 180	
ctg cag aat gct cat aat ggg gtc aac caa gcc agc aag gag gcc aac	628
Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser Lys Glu Ala Asn	
185 190 195	
cag ctg ctg aat ggc aac cat caa agc gga tct tcc agc cat caa gga	676
Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser Ser Ser His Gln Gly	
200 205 210 215	
ggg gcc aca acc aac cgg tta gcc tct ggg gcc tgg gtc aac aag cct	724
Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly Ala Ser Val Asn Thr Pro	
220 225 230	
ttc atc aac ctt ccc gcc ctg tgg agg agc gtc gcc aac atc atg ccc	772
Phe Ile Asn Leu Pro Ala Leu Trp Arg Ser Val Ala Asn Ile Met Pro	
235 240 245	
taaaactgg catcgggcct tctggggaga ataattgtgc cgttgctaca tcagctgaca	830
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 <12> DNA
 <13> Homo sapiens

<120>
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cctggggggtt gcc atg gcc ccc agc cae ctg tca gtg cgg gag atg agg	109
Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg	
1 5 10	
gaa gat gag aag ccc ctg gtg ctg gag atg ctg aag gcc ggc gtg aag	157
Glu Asp Glu Lys Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys	
15 20 25	
gac aag gaa aac cgg gtg gcc ctg cat gcc ttg aca cgg ccg ccg gcc	205
Asp Thr Glu Asn Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala	
30 35 40	
ctg ctg ctg ctg gcc gcc gcc agc agc ggc ctg cgc ttt gtc ctg gct	253
Leu Leu Leu Leu Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala	
45 50 55 60	
tcc ttc gcc ctg gcc ctg ctg ctg cgg gtg ttc ctg gct gtg gcc gcc	301
Ser Phe Ala Leu Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala	
65 70 75	
gtg aag ctg ggc ctg cgg gcc cga tgg ggc tgg ctg cct ccg ccg ggt	349
Val Lys Leu Gly Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly	
80 85 90	
ggc ctg ggg gcc ccc tgg gtg gcc gtc cgg ggc tcc ggt gac gtg ttt	397
Gly Leu Gly Gly Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys	

95	100	105	
ggg gtc ctg gct ctg gcc cct ggc aca aat gca ggg gac ggg gcc cgg			445
Gly Val Leu Ala Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg			
110	115	120	
gtc acc cgc ctg tct gtc tct cgc tgg cac cgc cgc cgg ggc gtg ggc			493
Val Thr Arg Leu Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly			
125	130	135	140
agg agg ctg ctg gcc ttc ggc gag gcc cgg gct cgg gcc tgg gct ggg			541
Arg Arg Leu Leu Ala Phe Ala Glu Ala Arg Ala Arg Ala Trp Ala Gly			
145	150	155	
ggc atg ggg gag ccc cgg gcc cgg ctc gtg gtc ccc gtg gct gtg gcc			589
Gly Met Gly Glu Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala			
160	165	170	
gcc tgg ggg gtg gga ggg atg ctg gag gcc tgt gcc tac cag gcc gag			637
Ala Trp Gly Val Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu			
175	180	185	
ggg ggc tgg gcc tgc ctg ggc tac aag ctg gtg agg gaa ttc agc aaa			685
Gly Gly Trp Gly Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys			
190	195	200	
gac ctg tgaagctaca gactgacagc cagggcaggc gaggaggagg gggcgccag			740
Asp Leu			
205			
gacctgatga tggcctaactg ttctgggggtt cttttacctg ctctccctca gtgagtcctc			800
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 <213> Homo sapiens

 <220>
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 atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct ggc ttc ccc tcc 165
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15
 cta cgg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 213
 Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30
 cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct gcc tat gcc agc 261
 Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 ttt atg gta cct gcc tac ctc ctg gtg cag tac ttc agg cgg aag aac 309
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 357
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 gtg ttt gcc aat cag ccc aag gcc tct gat gag att ccc ctg ggc ccc 401

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro	85	90	95
cga aca gag ggg gca gag acc acc cgg atg tgg cag gcc ctg aag ctg			453
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu	100	105	110
ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg			501
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val	115	120	125
ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca			549
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser	130	135	140
cgg ggt gag cgc ttt acg gac tog cag ttc ctg gtg cta atg aac cga			597
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg	145	150	155
gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag			645
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln	165	170	175
ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc			693
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser	180	185	190
aat gtg ctc agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc			741
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser	195	200	205
ttc ccc acc cag gtg ctg gcc aag gcc tct aag ctg atc cct gtc atg			789
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met	210	215	220
ctg arg gga aag ctt gtg tct cgg cgc acc tac caa cac tgg gag tac			837
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Gln Tyr	225	230	235
ctg aca gcc aca ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc			885
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser	245	250	255
agg gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc			933
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu	260	265	270
atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg			981
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp	275	280	285
cag gat gcc ctg ttt gcc tat aag atg tca tog gtg cag atg atg ttt			1029
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe	290	295	300
ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa			1077
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu	305	310	315
cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag			1125
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu	325	330	335
ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt gcc cag			1173
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln	340	345	350
ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc			1221
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr	355	360	365
atc atc atg acc ctc ccc cag gcc ttt gcc atc ctt ctt tcc tgc ctt			1269
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu	370	375	380
ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg			1317
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val	385	390	395
gtc ttt gat gcc ctc ctg ctc aga gtc tac ggg cgg ggc ggt cta aag			1365
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys			

405	410	415	
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Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val			
420	425	430	
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ccagcaccac caa tcttat gctcctggat cccataggctc tgttccatga gctgtttgca			1950
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 <213> Homo sapiens

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Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu	
1 5 10	
ctg acc ttg tgg gtc act ggg ggg acc cgg gag gta tgg gta caa gtt	155
Leu Thr Leu Cys Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val	
15 20 25	
cgg atg gag gca acc gag ctg tgg tcc ttc acc atc cgt tgt ggg ttc	206
Arg Met Glu Ala Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe	
30 35 40	
ctg ggg tct ggg tcc atc tcc ctg gta act gta agc tgg ggg ggc ccc	254
Leu Gly Ser Gly Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro	
45 50 55 60	
gac ggt gct ggg ggg acc acg ctg gct gta tgg cac cca gaa cgt ggc	302
Asp Gly Ala Gly Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly	
65 70 75	
atc cgg caa tgg gcc cct gct cgc cag gcc cgc tgg gaa acc cag agc	350
Ile Arg Gln Trp Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser	
80 85 90	
agc atc tct ctg atc ctg gaa ggc tct ggg gcc agc agc ccc tgc gcc	398
Ser Ile Ser Leu Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala	
95 100 105	
aac acc acc ttg tgc tgc aag ttt ggc tcc ttc cct gag ggc tcc tgg	446
Asn Thr Thr Phe Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp	
110 115 120	
gag gcc tgt ggg agc ctg cgg ccc agc tca gac cca cgg ctg tct gcc	494
Glu Ala Cys Gly Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala	
125 130 135 140	
cgg cgg act cct gcc ccc att ctg cgg gca gac ctg gcc ggg atc ttg	542
Pro Pro Thr Pro Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu	
145 150 155	
ggg gta tca gga gta ctg ctg ttt ggc tgt gta taa ctg ctt cat ctg	590
Gly Val Ser Gly Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu	
160 165 170	
ctg cgc cga cat aag cac cgc cct gcc cct agc ctg cag cgt tcc ggc	638

Leu Arg Arg His Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg
 175 180 185
 acc agc ccc cag gca ccg aga gca cga gca tgg gca cca agc cag gcc 686
 Thr Ser Pro Gln Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala
 190 195 200
 tcc cag gct gct ctt cac gtc cct tat gcc act atc aac acc agc tgc 734
 Ser Gln Ala Ala Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys
 205 210 215 220
 gcc cca gct act ttg gac aca gct cac ccc cat ggg ggg ccg tcc tgg 782
 Arg Pro Ala Thr Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp
 225 230 235
 tgg gcg tca ctc ccc acc cac gct gca cac cgg ccc cag gcc cct gcc 830
 Trp Ala Ser Leu Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala
 240 245 250
 gcc tgg gcc tcc aca ccc atc cct gca cgt gcc agc ttt gtc tct gtt 878
 Ala Trp Ala Ser Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val
 255 260 265
 gag aat gga ctc tac gct cag gca ggg gag agg cct cct cac act ggt 926
 Gln Asn Gly Leu Tyr Ala Gln Ala Gly Glu Arg Pro Pro His Thr Gly
 270 275 280
 ccc ggc ctc act ctt ttc cct gac cct cgg ggg ccc agg gcc atg gaa 974
 Pro Gly Leu Thr Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu
 285 290 295 300
 gga ccc tta gga gtt cga tgagagagac catgaggcca ctgggctt 1020
 Gly Pro Leu Gly Val Arg
 305

taccctctcc aggcctcctg gggtgcaccc ccttaacttta attcttgggc ccccaataag 1080
 tctcccatag gtgtctggcc aggccacct gctggcgatg tggctgtgtt ggtgtgtgg 1140
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 agtcagcaac acagtttctc tgatgtc 1227

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 ggccgagacc ggagcgcgcg tcgcgcgaga cttacttccc cggctcagca gggaaagggt 180
 ctadaaggt gagcgggac ggt atg caa agt tgt gaa tcc agt ggt gac agt 233
 Met Gln Ser Cys Glu Ser Ser Gly Asp Ser
 1 5 10
 jcg gat gac cct ctc agt cgc gcc cta cgg aga agg gga cag cct cgt 281
 Ala Asp Asp Pro Leu Ser Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg
 15 20 25
 jtg gtg gtg atc gcc gcc gcc ttg gct gcc ctg gct gca gcc aaa gca 329
 Val Val Val Ile Gly Ala Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala
 30 35 40
 ctt ctt gag cag ggt ttc aag gat gtc act gtg ctt gag gct tcc agc 377
 Leu Leu Glu Gln Gly Phe Thr Asp Val Thr Val Leu Glu Ala Ser Ser
 45 50 55
 cac atc gga gcc cgt gtg cag agt gtg aaa ctt gga cac gcc acc ttt 425
 His Ile Gly Gly Arg Val Gln Ser Val Lys Leu Gly His Ala Thr Phe
 60 65 70
 gag atg gga gcc acc tgg atc cat gcc tcc cat ggg aat cat atc tat 473
 Glu Leu Gly Ala Thr Trp Ile His Gly Ser His Gly Asn Pro Ile Tyr

75	80	85	90	
cat cta gca gaa gcc aac ggc ctc ctg gaa gag aca acc gat ggg gaa				521
His Leu Ala Glu Ala Asn Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu				
	95	100	105	
cgc agc gtg ggc cgc atc agc ctc tat tcc aag aat ggc gtg gcc tgc				569
Arg Ser Val Gly Arg Ile Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys				
	110	115	120	
tac ctt acc aac cac ggc cgc agg atc ccc aag gac gtg gtt gag gaa				617
Tyr Leu Thr Asn His Gly Arg Arg Ile Pro Lys Asp Val Val Glu Glu				
	125	130	135	
ttc agc gat tta tac aac gag gtc tat aac ttg acc cag gag ttc ttc				665
Phe Ser Asp Leu Tyr Asn Glu Val Tyr Asn Leu Thr Gln Glu Phe Phe				
	140	145	150	
cgg cac gat aaa cca gtc aat gct gaa agt caa aat agc gtg ggg gtg				713
Arg His Asp Lys Pro Val Asn Ala Glu Ser Gln Asn Ser Val Gly Val				
	155	160	165	170
ttc acc cga gag gag gtg cgt aac cgc atc agg aat gac cct gac gac				761
Phe Thr Arg Glu Gln Val Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp				
	175	180	185	
cca gag gct acc aag cgc ctg aag ctc gcc atg atc cag cag tac ctg				809
Pro Glu Ala Thr Lys Arg Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu				
	190	195	200	
aag gtg gag agc tgt gag agc agc tca cac agc atg gac gag gtg tcc				857
Lys Val Glu Ser Cys Glu Ser Ser Ser His Ser Met Asp Glu Val Ser				
	205	210	215	
ctg agc gcc ttc ggg gag tgg acc gag atc ccc ggc gct cac cac atc				905
Leu Ser Ala Phe Gly Gln Trp Thr Glu Ile Pro Gly Ala His His Ile				
	220	225	230	
atc ccc tgg ggc ttc atg cgg gtt gtg gag ctg ctg gcc gag gcc atc				953
Ile Pro Ser Gly Phe Met Arg Val Val Glu Leu Leu Ala Glu Gly Ile				
	235	240	245	250
cct gcc cac gtc atc cag cca ggg aaa cct gtc cgc tgc att cac tgg				1001
Pro Ala His Val Ile Gln Leu Gly Lys Pro Val Arg Cys Ile His Trp				
	255	260	265	
gac cag gcc tca gcc cgc ccc aga ggc cct gag att gag ccc cgg ggt				1049
Asp Gln Ala Ser Ala Arg Pro Arg Gly Pro Glu Ile Glu Pro Arg Gly				
	270	275	280	
gag ggc gac cac aat cac gac aot ggg gag ggt ggc cag ggt gga gag				1097
Glu Gly Asp His Asn His Asp Thr Gly Glu Gly Gly Gln Gly Gly Glu				
	285	290	295	
gag ccc cgg ggg ggc agg tgg gat gag gat gag cag tgg tgg gtg gtg				1145
Glu Pro Arg Gly Gly Arg Trp Asp Glu Asp Glu Gln Trp Ser Val Val				
	300	305	310	
gtg gag tgc gag gac tgt gag ctg atc ccc gcc gac cat gtg att gtg				1193
Val Glu Cys Glu Asp Cys Gln Leu Ile Pro Ala Asp His Val Ile Val				
	315	320	325	330
acc gtg tgg cta ggt gtg cta aag agg cag tac acc agt ttc ttc cgg				1241
Thr Val Ser Leu Gly Val Leu Lys Arg Gln Tyr Thr Ser Phe Phe Arg				
	335	340	345	
cca ggc ctg ccc aca gag aag gtg gct gcc atc cac cgc ctg gcc att				1289
Pro Gly Leu Pro Thr Glu Lys Val Ala Ala Ile His Arg Leu Gly Ile				
	350	355	360	
ggc acc acc gac aag atc ttt ctg gaa ttc gag gag ccc ttc tgg gcc				1337
Gly Thr Thr Asp Lys Ile Phe Leu Glu Phe Glu Glu Pro Phe Trp Gly				
	365	370	375	
cct gag tgc aac agc cta cag ttt gtg tgg gag gac gaa gcc gag agc				1385
Pro Glu Cys Asn Ser Leu Gln Phe Val Trp Glu Asp Glu Ala Glu Ser				
	380	385	390	
cac acc ctc acc tac cca cct gag ctg tgg tac cgc aag atc tgc gcc				1433
His Thr Leu Thr Tyr Pro Pro Glu Leu Trp Tyr Arg Lys Ile Cys Gly				
	395	400	405	410

ttt gat gtc ctc tac ccg cct gag cgc tac ggc cat gtg ctg agc ggc	1481
Phe Asp Val Leu Tyr Pro Pro Glu Arg Tyr Gly His Val Leu Ser Gly	
415 420 425	
tgg atc tgc ggg gag gag gcc ctc gtc atg gag aag tgt gat gac gag	1529
Trp Ile Cys Gly Glu Glu Ala Leu Val Met Glu Lys Cys Asp Asp Glu	
430 435 440	
gca gtg gcc gag atc tgc acg gag atg ctg cgt cag ttc aca ggg aac	1577
Ala Val Ala Glu Ile Cys Thr Glu Met Leu Arg Gln Phe Thr Gly Asn	
445 450 455	
ccc aac att cca aaa cct cgg cga atc ttg cgc tgg gcc tgg ggc agc	1625
Pro Asn Ile Pro Lys Pro Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser	
460 465 470	
aac cct tac ttc cgc ggc tcc tat tca tac acg cag gtg ggc tcc agc	1673
Asn Pro Tyr Phe Arg Gly Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser	
475 480 485 490	
ggg cgc gat gtg gag aag ctg gcc aag ccc ctg cgg tac acg gag agc	1721
Gly Ala Asp Val Glu Lys Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser	
495 500 505	
tca aag aca ggc ccc atg cag gtg ctg ttt tcc ggt gag gcc acc cac	1769
Ser Lys Thr Ala Pro Met Gln Val Leu Phe Ser Gly Glu Ala Thr His	
510 515 520	
cgt aag tac tat tcc acc acc cag ggt gct ctg ctg tcc ggc cag cgt	1817
Arg Lys Tyr Tyr Ser Thr Thr His Gly Ala Leu Leu Ser Gly Gln Arg	
525 530 535	
gag cct gcc cgc ctc att gag atg tac cga gac ctc ttc cag cag ggg	1865
Glu Ala Ala Arg Leu Ile Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly	
540 545 550	
aaa tggagggtgt cctcgtgtgt gagaagagcc actaac tgc gacatcaggt ca	1920
Thr	
555	
gacatctgtt ggcgtgtgtt cctgcctctcc tgcctctctg tagaaaggat ttttatcttc	1980
tgcagagcta gccgccttga ctgccttcag acctggcctt gtagcttttc tttttctcca	2040
ggctgggccc tgagcaggtg gccgcttgag ttaacctctt gctggatccc gtgcctccac	2100
tgcctaccc tctgctctga ctgtttattg taagtgcctt caatacttg cattttggga	2160
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gagggacatg acaccagtgg catatcacgg ca atg ggg tct cag cat tcc gct	113
Met Gly Ser Gln His Ser Ala	
1 5	
gct cct cgc ccc tcc tcc tgc agg cga aag caa gaa gat gac agg gac	161
Ala Ala Arg Pro Ser Ser Cys Arg Arg Lys Gln Glu Asp Asp Arg Asp	
10 15 20	
ggc ttg ctg gct gaa cga gag cag gaa gaa gcc att gct cag ttc cca	209
Gly Leu Leu Ala Glu Arg Glu Gln Glu Glu Ala Ile Ala Gln Phe Pro	
25 30 35	
tat gtg gaa ttc acc ggg aga gat agc atc acc tgt ctc acg tgc cag	257
Tyr Val Glu Phe Thr Gly Arg Asp Ser Ile Thr Cys Leu Thr Cys Gln	
40 45 50 55	
ggt aca ggc tac att cca aca gag caa gta aat gag ttg gta gct ttg	305
Gly Thr Gly Tyr Ile Pro Thr Glu Gln Val Asn Glu Leu Val Ala Leu	

60	65	70	
atc cca cac apt gat cag aga ttg cgc cct cag cga act aag caa tat			353
Ile Pro His Ser Asp Gln Arg Leu Arg Pro Gln Arg Thr Lys Gln Tyr			
75	80	85	
gtc ctg ctg tcc atc ctg ctt tgt ctc cta gca tct ggt ttg gtg gtt			401
Val Leu Leu Ser Ile Leu Leu Cys Leu Leu Ala Ser Gly Leu Val Val			
90	95	100	
ttc ttc ctg ttc cag cat tca gtc ctt gtg gat gat gac ggc atc aaa			449
Phe Phe Leu Phe Pro His Ser Val Leu Val Asp Asp Gly Ile Lys			
105	110	115	
gtg gtg aaa gtc aca ttt aat aag caa gar tcc ctt gta att ctc acc			497
Val Val Lys Val Thr Phe Asn Lys Gln Asp Ser Leu Val Ile Leu Thr			
120	125	130	135
atc atg gcc acc ctg aaa atc agg aac tcc aac ttc tac acg gtg gca			545
Ile Met Ala Thr Leu Lys Ile Arg Asn Ser Asn Phe Tyr Thr Val Ala			
140	145	150	
gtg acc agc ctg tcc agc cag att cag tac atg aac aca gtg gtc agt			593
Val Thr Ser Leu Ser Ser Gln Ile Gln Tyr Met Asn Thr Val Val Ser			
155	160	165	
aca tat gtg act act aac gtc tcc ctt att cca cct cgg agt gag caa			641
Thr Tyr Val Thr Thr Asn Val Ser Leu Ile Pro Pro Arg Ser Glu Gln			
170	175	180	
ctg gtg aat ttt acc ggg aag gcc gag atg gga gga cgg ttt tcc tat			689
Leu Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly Pro Phe Ser Tyr			
185	190	195	
gtg tac ttc ttc tgc acc gta cct gag atc ctg gtg cag aac ata gtg			737
Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val His Asn Ile Val			
200	205	210	215
atc ttc atg cca act tca gtg aag att tca tac att ggc ctc atg acc			785
Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile Gly Leu Met Thr			
220	225	230	
cag agc tcc ttg gag aca cat cac tal gtg gat tgt gga gga aat tcc			833
Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys Gly Gly Asn Ser			
235	240	245	
aca gct att taacaaactgc tattgggttct tccacacagc gcctgtagaa gagagcac			890
Thr Ala Ile			
250			
agcatatggtt cccaaggcct gagttctgga cctaccccca cgtggtgttaa gcagaggagg			950
aattggttca ctttaactccc agcaaacatc ctctgtccac ttaggaggaa acacctccct			1010
atggtaccat ttatgtttct cagaaccagc agaattcagt cctagcctgt gccacgcaaa			1070
tagttagcac tcaataaaga ttgcagaat ttaatacaga tcttttcagc tgtttcttagg			1130
gcattataaaa tggaaatcat aacgtgggtc taggttatca aaccatggag tgatgtggag			1190
ctaggattgt gactgaactg caggccatta tcaagtgcctc atctgtgcag aagtcgcagc			1250
agagagggac catccaaata cctaagagaa aacagacctc gtcaggatat gaatttgttt			1310
cagctgttcc caaaggcctg ggagcttttt gaaaagaaag aaaaaagtgt gttggctttt			1370
ttttttttta gaaagttaga attgttttta ccaagagttc atgtggggct tgattcaccc			1430
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ttc			1493

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<220>
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<400> 150
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 Met Gln Ala Pro Ala Phe Arg Asp Lys

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aaa cag ggg gtc tca gcc aag aat caa ggt gcc cat gac cca gac tat			100
Lys Gln Gly Val Ser Ala Lys Asn Gln Gly Ala His Asp Pro Asp Tyr			
10 15 20 25			
gag aat atc acc ttg gcc ttc aaa aat cag gac cat gca aag ggt ggt			148
Glu Asn Ile Thr Leu Ala Phe Lys Asn Gln Asp His Ala Lys Gly Gly			
30 35 40			
cat tca cga ccc acg agc caa gtc cca gcc cag tgc agg ccg ccc tca			196
His Ser Arg Pro Thr Ser Gln Val Pro Ala Gln Cys Arg Pro Ser			
45 50 55			
gac tcc acc cag gtc ccc tgc tgg ttg tac aga gcc atc ctg agc ctg			244
Asp Ser Thr Gln Val Pro Cys Trp Leu Tyr Arg Ala Ile Leu Ser Leu			
60 65 70			
tac atc ctg ctg gcc ctg gcc ttt gtc ctg tgc atc atc ctg tca gcc			292
Tyr Ile Leu Leu Ala Leu Ala Phe Val Leu Cys Ile Ile Leu Ser Ala			
75 80 85			
ttc atc atg gtg aag aat ggt gag atg tcc aag gag ctg ctg ggc ttt			340
Phe Ile Met Val Lys Asn Ala Gln Met Ser Lys Glu Leu Leu Gly Phe			
90 95 100 105			
aaa agg gag ctt tgg aat gtc tca aac tcc gta caa gca tgc gaa gag			388
Lys Arg Glu Leu Trp Asn Val Ser Asn Ser Val Gln Ala Cys Gln Gln			
110 115 120			
aga cag aag aga gcc tgg gat tcc gtt cag cag agc atc acc atg gtc			436
Arg Gln Lys Arg Gly Trp Asp Ser Val Gln Gln Ser Ile Thr Met Val			
125 130 135			
agg agc aag att gat aga tta gag acg aca tta gca gcc ata aaa aac			484
Arg Ser Lys Ile Asp Arg Leu Gln Thr Thr Leu Ala Gly Ile Lys Asn			
140 145 150			
att gac aca aag gta cag aaa atc ttg gag gtg ctg cag aca atg cca			532
Ile Asp Thr Lys Val Gln Lys Ile Leu Glu Val Leu Gln Lys Met Pro			
155 160 165			
cag tcc tca cct caa taaatgagag gacattgttg cagccaaagc cac			580
Gln Ser Ser Pro Gln			
170			
aacttgggaag atgggggtgc aactgccaac gaagacggga aatgaccccc ccccccagcc			640
tagtgtgaac ctgcccctcg tccacgtat agaaaaacct cgagtcctgg tgaatgagtg			700
tctggagatt gctgtgtgt gtgtacaccc gctgctgtgt gtgtgctgt gtgctgtgt			760
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cagtgtatct cccagaaagg tgatgaatga ataggactga gactcacagt gaatgtggca			880
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tgagcacctc cagcagatgt cactctgagt gtgggtgtttg gtgacatgca ttgcacgggc			1000
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tgtcagggc acatgcacac agacatttat ctctgcactc acattttgtg acctatgaag			1240
ataaataaag tcaagggaac acag			1264